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SEQUENCE LISTING

<110> Wolfrain, Lawrence A
Letterio, John J

<120> FUNCTIONALIZED TGF-BETA FUSION PROTEINS

<130> 4239-61302

<140> US 10/017,372

<141> 2001-10-19

<150> US 60/242,292

<151> 2000-10-20

<160> 39

<170> PatentIn version 3.2

<210> 1

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 1

ggagagatct ggtaccgaga tggcgctt

28

<210> 2

<211> 42

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 2

ataagaattg cggccgcttt aatcgatccc aagtgggctt gg

42

<210> 3

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 3

gactacaagg atgacgacga caaggccctg gataccaact actgcttc

48

<210> 4

<211> 45

<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 4
cttgctgctg tcatccttgt agtctcggcg gtgccgggag ctgtg 45

<210> 5
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 5
gactacaagg atgacgacga caggagaaga actgctgcgt gcggc 45

<210> 6
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 6
cttgctgctg tcatccttgt agtctcggcg gtgccgggag ctgtg 45

<210> 7
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic oligopeptide

<400> 7
Asp Tyr Lys Asp Asp Asp Asp Lys
1 5

<210> 8
<211> 1197
<212> DNA
<213> Artificial Sequence

<220>
<223> Porcine (Sus scrofa) TGF-beta1/N-terminal FLAG Fusion Construct

<220>
 <221> CDS
 <222> (1)..(1197)
 <223> Protein coding sequence

<220>
 <221> misc_feature
 <222> (278)..(279)
 <223> Maturation cleavage site (relates to amino acid residue nos.)

<400> 8
 atg gcg cct tcg ggg ctg cgg ctc ttg ccg ctg ctg ctg ccg ctg ctg 48
 Met Ala Pro Ser Gly Leu Arg Leu Leu Pro Leu Leu Leu Pro Leu Leu
 1 5 10 15

tgg ctg cta gtg ctg acg cct ggc cgg ccg gcc gcc gga ctg tcc acc 96
 Trp Leu Leu Val Leu Thr Pro Gly Arg Pro Ala Ala Gly Leu Ser Thr
 20 25 30

tgc aag acc atc gac atg gag ctg gtg aag cgg aag cgc atc gag gcc 144
 Cys Lys Thr Ile Asp Met Glu Leu Val Lys Arg Lys Arg Ile Glu Ala
 35 40 45

att cgc ggc cag att ctg tcc aag ctt cgg ctt gcc agc ccc ccg agc 192
 Ile Arg Gly Gln Ile Leu Ser Lys Leu Arg Leu Ala Ser Pro Pro Ser
 50 55 60

cag ggg gac gtg ccg ccc ggc ccg ctg cct gag gca gta ctg gct ctt 240
 Gln Gly Asp Val Pro Pro Gly Pro Leu Pro Glu Ala Val Leu Ala Leu
 65 70 75 80

tac aac agt acc cgc gac cgg gta gcc ggg gaa agt gtc gaa ccg gag 288
 Tyr Asn Ser Thr Arg Asp Arg Val Ala Gly Glu Ser Val Glu Pro Glu
 85 90 95

ccc gag cca gag gcg gac tac, tac gcc aag gag gtc acc cgc gtg cta 336
 Pro Glu Pro Glu Ala Asp Tyr Tyr Ala Lys Glu Val Thr Arg Val Leu
 100 105 110

atg gtg gaa agc ggc aac caa atc tat gat aaa ttc aag ggc acc ccc 384
 Met Val Glu Ser Gly Asn Gln Ile Tyr Asp Lys Phe Lys Gly Thr Pro
 115 120 125

cac agc tta tat atg ctg ttc aac acg tcg gag ctc cgg gaa gcg gtg 432
 His Ser Leu Tyr Met Leu Phe Asn Thr Ser Glu Leu Arg Glu Ala Val
 130 135 140

ccg gaa cct gta ttg ctc tct cgg gca gag ctg cgc ctg ctg agg ctc 480
 Pro Glu Pro Val Leu Leu Ser Arg Ala Glu Leu Arg Leu Leu Arg Leu
 145 150 155 160

aag tta aaa gtg gag cag cac gtg gag cta tac cag aaa tac agc aat 528
 Lys Leu Lys Val Glu Gln His Val Glu Leu Tyr Gln Lys Tyr Ser Asn
 165 170 175

gat tcc tgg cgc tac ctc agc aac cgg ctg ctg gcc ccc agt gac tca 576
 Asp Ser Trp Arg Tyr Leu Ser Asn Arg Leu Leu Ala Pro Ser Asp Ser

180	185	190	
ccg gag tgg ctg tcc ttt gat gtc acc gga gtt gtg cgg cag tgg ctg			624
Pro Glu Trp Leu Ser Phe Asp Val Thr Gly Val Val Arg Gln Trp Leu			
195	200	205	
acc cgc aga gag gct ata gag ggt ttt cgc ctc agt gcc cac tct tcc			672
Thr Arg Arg Glu Ala Ile Glu Gly Phe Arg Leu Ser Ala His Ser Ser			
210	215	220	
tct gac agc aaa gat aac aca ctc cac gtg gaa att aac ggg ttc aat			720
Ser Asp Ser Lys Asp Asn Thr Leu His Val Glu Ile Asn Gly Phe Asn			
225	230	235	240
tct ggc cgc cgg ggt gac ctg gcc acc att cac ggc atg aac cgg ccc			768
Ser Gly Arg Arg Gly Asp Leu Ala Thr Ile His Gly Met Asn Arg Pro			
	245	250	255
ttc ctg ctc ctc atg gcc acc ccg ctg gag agg gcc cag cac ctg cac			816
Phe Leu Leu Leu Met Ala Thr Pro Leu Glu Arg Ala Gln His Leu His			
	260	265	270
agc tcc cgg cac cgc cga gac tac aag gat gac gac gac aag gcc ctg			864
Ser Ser Arg His Arg Arg Asp Tyr Lys Asp Asp Asp Asp Lys Ala Leu			
	275	280	285
gat acc aac tac tgc ttc agc tcc acg gag aag aac tgc tgc gtg cgg			912
Asp Thr Asn Tyr Cys Phe Ser Ser Thr Glu Lys Asn Cys Cys Val Arg			
	290	295	300
cag ctc tac att gac ttc cgg aag gac ctg ggc tgg aag tgg att cat			960
Gln Leu Tyr Ile Asp Phe Arg Lys Asp Leu Gly Trp Lys Trp Ile His			
305	310	315	320
gaa ccc aag ggc tac cat gcc aat ttc tgc ctg ggg ccc tgt ccc tac			1008
Glu Pro Lys Gly Tyr His Ala Asn Phe Cys Leu Gly Pro Cys Pro Tyr			
	325	330	335
atc tgg agc cta gac act cag tac agc aag gtc ctg gct ctg tac aac			1056
Ile Trp Ser Leu Asp Thr Gln Tyr Ser Lys Val Leu Ala Leu Tyr Asn			
	340	345	350
cag cac aac ccg ggc gcg tcg gcg gcg ccg tgc tgc gtg ccg cag gcg			1104
Gln His Asn Pro Gly Ala Ser Ala Ala Pro Cys Cys Val Pro Gln Ala			
	355	360	365
ctg gag cca ctg ccc atc gtg tac tac gtg ggc cgc aag ccc aag gtg			1152
Leu Glu Pro Leu Pro Ile Val Tyr Tyr Val Gly Arg Lys Pro Lys Val			
	370	375	380
gag cag ctg tcc aac atg atc gtg cgt tcc tgc aag tgc agc tga			1197
Glu Gln Leu Ser Asn Met Ile Val Arg Ser Cys Lys Cys Ser			
385	390	395	

<210> 9
<211> 398

<212> PRT

<213> Artificial Sequence

<220>

<223> Porcine (Sus scrofa) TGF-beta1/N-terminal FLAG Fusion Construct

<400> 9

Met Ala Pro Ser Gly Leu Arg Leu Leu Pro Leu Leu Leu Pro Leu Leu
1 5 10 15

Trp Leu Leu Val Leu Thr Pro Gly Arg Pro Ala Ala Gly Leu Ser Thr
20 25 30

Cys Lys Thr Ile Asp Met Glu Leu Val Lys Arg Lys Arg Ile Glu Ala
35 40 45

Ile Arg Gly Gln Ile Leu Ser Lys Leu Arg Leu Ala Ser Pro Pro Ser
50 55 60

Gln Gly Asp Val Pro Pro Gly Pro Leu Pro Glu Ala Val Leu Ala Leu
65 70 75 80

Tyr Asn Ser Thr Arg Asp Arg Val Ala Gly Glu Ser Val Glu Pro Glu
85 90 95

Pro Glu Pro Glu Ala Asp Tyr Tyr Ala Lys Glu Val Thr Arg Val Leu
100 105 110

Met Val Glu Ser Gly Asn Gln Ile Tyr Asp Lys Phe Lys Gly Thr Pro
115 120 125

His Ser Leu Tyr Met Leu Phe Asn Thr Ser Glu Leu Arg Glu Ala Val
130 135 140

Pro Glu Pro Val Leu Leu Ser Arg Ala Glu Leu Arg Leu Leu Arg Leu
145 150 155 160

Lys Leu Lys Val Glu Gln His Val Glu Leu Tyr Gln Lys Tyr Ser Asn
165 170 175

Asp Ser Trp Arg Tyr Leu Ser Asn Arg Leu Leu Ala Pro Ser Asp Ser
180 185 190

Pro Glu Trp Leu Ser Phe Asp Val Thr Gly Val Val Arg Gln Trp Leu

195

200

205

Thr Arg Arg Glu Ala Ile Glu Gly Phe Arg Leu Ser Ala His Ser Ser
 210 215 220

Ser Asp Ser Lys Asp Asn Thr Leu His Val Glu Ile Asn Gly Phe Asn
 225 230 235 240

Ser Gly Arg Arg Gly Asp Leu Ala Thr Ile His Gly Met Asn Arg Pro
 245 250 255

Phe Leu Leu Leu Met Ala Thr Pro Leu Glu Arg Ala Gln His Leu His
 260 265 270

Ser Ser Arg His Arg Arg Asp Tyr Lys Asp Asp Asp Asp Lys Ala Leu
 275 280 285

Asp Thr Asn Tyr Cys Phe Ser Ser Thr Glu Lys Asn Cys Cys Val Arg
 290 295 300

Gln Leu Tyr Ile Asp Phe Arg Lys Asp Leu Gly Trp Lys Trp Ile His
 305 310 315 320

Glu Pro Lys Gly Tyr His Ala Asn Phe Cys Leu Gly Pro Cys Pro Tyr
 325 330 335

Ile Trp Ser Leu Asp Thr Gln Tyr Ser Lys Val Leu Ala Leu Tyr Asn
 340 345 350

Gln His Asn Pro Gly Ala Ser Ala Ala Pro Cys Cys Val Pro Gln Ala
 355 360 365

Leu Glu Pro Leu Pro Ile Val Tyr Tyr Val Gly Arg Lys Pro Lys Val
 370 375 380

Glu Gln Leu Ser Asn Met Ile Val Arg Ser Cys Lys Cys Ser
 385 390 395

<210> 10

<211> 363

<212> DNA

<213> Artificial Sequence

<220>

<223> Porcine (Sus scrofa) TGF-beta1/N-terminal FLAG Fusion Construct

<400> 10
gactacaagg atgacgacga caaggccctg gataccaact actgcttcag ctccacggag 60
aagaactgct gcgtgcggca gctctacatt gacttccgga aggacctggg ctggaagtgg 120
attcatgaac ccaagggcta ccatgccaat ttctgcctgg ggccctgtcc ctacatctgg 180
agcctagaca ctcagtacag caaggctctg gctctgtaca accagcaciaa cccggggcgcg 240
tcggcggcgc cgtgctgcgt gccgcaggcg ctggagccac tgcccatcgt gtactacgtg 300
ggcgcgaagc ccaaggtgga gcagctgtcc aacatgatcg tgcgttcctg caagtgcagc 360
tga 363

<210> 11
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> Porcine (Sus scrofa) TGF-beta1/N-terminal FLAG Fusion Construct

C1
<220>
<221> PEPTIDE
<222> (1)..(8)
<223> FLAG tag

<400> 11

Asp Tyr Lys Asp Asp Asp Asp Lys Ala Leu Asp Thr Asn Tyr Cys Phe
1 5 10 15

Ser Ser Thr Glu Lys Asn Cys Cys Val Arg Gln Leu Tyr Ile Asp Phe
20 25 30

Arg Lys Asp Leu Gly Trp Lys Trp Ile His Glu Pro Lys Gly Tyr His
35 40 45

Ala Asn Phe Cys Leu Gly Pro Cys Pro Tyr Ile Trp Ser Leu Asp Thr
50 55 60

Gln Tyr Ser Lys Val Leu Ala Leu Tyr Asn Gln His Asn Pro Gly Ala
65 70 75 80

Ser Ala Ala Pro Cys Cys Val Pro Gln Ala Leu Glu Pro Leu Pro Ile
85 90 95

Val Tyr Tyr Val Gly Arg Lys Pro Lys Val Glu Gln Leu Ser Asn Met
 100 105 110

Ile Val Arg Ser Cys Lys Cys Ser
 115 120

<210> 12
 <211> 1197
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Porcine (Sus scrofa) TGF-beta1/FLAG (11/12) Fusion Construct

<220>
 <221> CDS
 <222> (1)..(1197)
 <223> Protein coding sequence

<220>
 <221> misc_feature
 <222> (278)..(279)
 <223> Maturation cleavage site (relates to amino acid residue nos.)

C1
 <400> 12
 atg gcg cct tcg ggg ctg cgg ctc ttg ccg ctg ctg ctg ccg ctg ctg 48
 Met Ala Pro Ser Gly Leu Arg Leu Leu Pro Leu Leu Leu Pro Leu Leu
 1 5 10 15
 tgg ctg cta gtg ctg acg cct ggc cgg ccg gcc gcc gga ctg tcc acc 96
 Trp Leu Leu Val Leu Thr Pro Gly Arg Pro Ala Ala Gly Leu Ser Thr
 20 25 30
 tgc aag acc atc gac atg gag ctg gtg aag cgg aag cgc atc gag gcc 144
 Cys Lys Thr Ile Asp Met Glu Leu Val Lys Arg Lys Arg Ile Glu Ala
 35 40 45
 att cgc ggc cag att ctg tcc aag ctt cgg ctt gcc agc ccc ccg agc 192
 Ile Arg Gly Gln Ile Leu Ser Lys Leu Arg Leu Ala Ser Pro Pro Ser
 50 55 60
 cag ggg gac gtg ccg ccc ggc ccg ctg cct gag gca gta ctg gct ctt 240
 Gln Gly Asp Val Pro Pro Gly Pro Leu Pro Glu Ala Val Leu Ala Leu
 65 70 75 80
 tac aac agt acc cgc gac cgg gta gcc ggg gaa agt gtc gaa ccg gag 288
 Tyr Asn Ser Thr Arg Asp Arg Val Ala Gly Glu Ser Val Glu Pro Glu
 85 90 95
 ccc gag cca gag gcg gac tac tac gcc aag gag gtc acc cgc gtg cta 336
 Pro Glu Pro Glu Ala Asp Tyr Tyr Ala Lys Glu Val Thr Arg Val Leu
 100 105 110

atg gtg gaa agc ggc aac caa atc tat gat aaa ttc aag ggc acc ccc	384
Met Val Glu Ser Gly Asn Gln Ile Tyr Asp Lys Phe Lys Gly Thr Pro	
115 120 125	
cac agc tta tat atg ctg ttc aac acg tgc gag ctc cgg gaa gcg gtg	432
His Ser Leu Tyr Met Leu Phe Asn Thr Ser Glu Leu Arg Glu Ala Val	
130 135 140	
ccg gaa cct gta ttg ctc tct cgg gca gag ctg cgc ctg ctg agg ctc	480
Pro Glu Pro Val Leu Leu Ser Arg Ala Glu Leu Arg Leu Leu Arg Leu	
145 150 155 160	
aag tta aaa gtg gag cag cac gtg gag cta tac cag aaa tac agc aat	528
Lys Leu Lys Val Glu Gln His Val Glu Leu Tyr Gln Lys Tyr Ser Asn	
165 170 175	
gat tcc tgg cgc tac ctc agc aac cgg ctg ctg gcc ccc agt gac tca	576
Asp Ser Trp Arg Tyr Leu Ser Asn Arg Leu Leu Ala Pro Ser Asp Ser	
180 185 190	
ccg gag tgg ctg tcc ttt gat gtc acc gga gtt gtg cgg cag tgg ctg	624
Pro Glu Trp Leu Ser Phe Asp Val Thr Gly Val Val Arg Gln Trp Leu	
195 200 205	
acc cgc aga gag gct ata gag ggt ttt cgc ctc agt gcc cac tct tcc	672
Thr Arg Arg Glu Ala Ile Glu Gly Phe Arg Leu Ser Ala His Ser Ser	
210 215 220	
tct gac agc aaa gat aac aca ctc cac gtg gaa att aac ggg ttc aat	720
Ser Asp Ser Lys Asp Asn Thr Leu His Val Glu Ile Asn Gly Phe Asn	
225 230 235 240	
tct ggc cgc cgg ggt gac ctg gcc acc att cac ggc atg aac cgg ccc	768
Ser Gly Arg Arg Gly Asp Leu Ala Thr Ile His Gly Met Asn Arg Pro	
245 250 255	
ttc ctg ctc ctc atg gcc acc ccg ctg gag agg gcc cag cac ctg cac	816
Phe Leu Leu Leu Met Ala Thr Pro Leu Glu Arg Ala Gln His Leu His	
260 265 270	
agc tcc cgg cac cgc cga gcc ctg gat acc aac tac tgc ttc agc tcc	864
Ser Ser Arg His Arg Arg Ala Leu Asp Thr Asn Tyr Cys Phe Ser Ser	
275 280 285	
acg gac tac aag gat gac gac gac aag gag aag aac tgc tgc gtg cgg	912
Thr Asp Tyr Lys Asp Asp Asp Asp Lys Glu Lys Asn Cys Cys Val Arg	
290 295 300	
cag ctc tac att gac ttc cgg aag gac ctg ggc tgg aag tgg att cat	960
Gln Leu Tyr Ile Asp Phe Arg Lys Asp Leu Gly Trp Lys Trp Ile His	
305 310 315 320	
gaa ccc aag ggc tac cat gcc aat ttc tgc ctg ggg ccc tgt ccc tac	1008
Glu Pro Lys Gly Tyr His Ala Asn Phe Cys Leu Gly Pro Cys Pro Tyr	
325 330 335	
atc tgg agc cta gac act cag tac agc aag gtc ctg gct ctg tac aac	1056

Ile Trp Ser Leu Asp Thr Gln Tyr Ser Lys Val Leu Ala Leu Tyr Asn
 340 345 350

cag cac aac ccg ggc gcg tcg gcg gcg ccg tgc tgc gtg ccg cag gcg 1104
 Gln His Asn Pro Gly Ala Ser Ala Ala Pro Cys Cys Val Pro Gln Ala
 355 360 365

ctg gag cca ctg ccc atc gtg tac tac gtg ggc cgc aag ccc aag gtg 1152
 Leu Glu Pro Leu Pro Ile Val Tyr Tyr Val Gly Arg Lys Pro Lys Val
 370 375 380

gag cag ctg tcc aac atg atc gtg cgt tcc tgc aag tgc agc tga 1197
 Glu Gln Leu Ser Asn Met Ile Val Arg Ser Cys Lys Cys Ser
 385 390 395

<210> 13

<211> 398

<212> PRT

<213> Artificial Sequence

<220>

<223> Porcine (Sus scrofa) TGF-beta1/FLAG (11/12) Fusion Construct

<400> 13

Met Ala Pro Ser Gly Leu Arg Leu Leu Pro Leu Leu Leu Pro Leu Leu
 1 5 10 15

Trp Leu Leu Val Leu Thr Pro Gly Arg Pro Ala Ala Gly Leu Ser Thr
 20 25 30

Cys Lys Thr Ile Asp Met Glu Leu Val Lys Arg Lys Arg Ile Glu Ala
 35 40 45

Ile Arg Gly Gln Ile Leu Ser Lys Leu Arg Leu Ala Ser Pro Pro Ser
 50 55 60

Gln Gly Asp Val Pro Pro Gly Pro Leu Pro Glu Ala Val Leu Ala Leu
 65 70 75 80

Tyr Asn Ser Thr Arg Asp Arg Val Ala Gly Glu Ser Val Glu Pro Glu
 85 90 95

Pro Glu Pro Glu Ala Asp Tyr Tyr Ala Lys Glu Val Thr Arg Val Leu
 100 105 110

Met Val Glu Ser Gly Asn Gln Ile Tyr Asp Lys Phe Lys Gly Thr Pro
 115 120 125

His Ser Leu Tyr Met Leu Phe Asn Thr Ser Glu Leu Arg Glu Ala Val
130 135 140

Pro Glu Pro Val Leu Leu Ser Arg Ala Glu Leu Arg Leu Leu Arg Leu
145 150 155 160

Lys Leu Lys Val Glu Gln His Val Glu Leu Tyr Gln Lys Tyr Ser Asn
165 170 175

Asp Ser Trp Arg Tyr Leu Ser Asn Arg Leu Leu Ala Pro Ser Asp Ser
180 185 190

Pro Glu Trp Leu Ser Phe Asp Val Thr Gly Val Val Arg Gln Trp Leu
195 200 205

Thr Arg Arg Glu Ala Ile Glu Gly Phe Arg Leu Ser Ala His Ser Ser
210 215 220

Ser Asp Ser Lys Asp Asn Thr Leu His Val Glu Ile Asn Gly Phe Asn
225 230 235 240

Ser Gly Arg Arg Gly Asp Leu Ala Thr Ile His Gly Met Asn Arg Pro
245 250 255

Phe Leu Leu Leu Met Ala Thr Pro Leu Glu Arg Ala Gln His Leu His
260 265 270

Ser Ser Arg His Arg Arg Ala Leu Asp Thr Asn Tyr Cys Phe Ser Ser
275 280 285

Thr Asp Tyr Lys Asp Asp Asp Asp Lys Glu Lys Asn Cys Cys Val Arg
290 295 300

Gln Leu Tyr Ile Asp Phe Arg Lys Asp Leu Gly Trp Lys Trp Ile His
305 310 315 320

Glu Pro Lys Gly Tyr His Ala Asn Phe Cys Leu Gly Pro Cys Pro Tyr
325 330 335

Ile Trp Ser Leu Asp Thr Gln Tyr Ser Lys Val Leu Ala Leu Tyr Asn
340 345 350

Gln His Asn Pro Gly Ala Ser Ala Ala Pro Cys Cys Val Pro Gln Ala
 355 360 365

Leu Glu Pro Leu Pro Ile Val Tyr Tyr Val Gly Arg Lys Pro Lys Val
 370 375 380

Glu Gln Leu Ser Asn Met Ile Val Arg Ser Cys Lys Cys Ser
 385 390 395

<210> 14
 <211> 363
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Porcine (Sus scrofa) TGF-beta1/FLAG (11/12) Fusion Construct

<400> 14
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 aagaactgct gcgtgcggca gctctacatt gacttccgga aggacctggg ctggaagtgg 120
 attcatgaac ccaagggcta ccatgccaat ttctgcctgg ggccctgtcc ctacatctgg 180
 agcctagaca ctcagtacaa caaggtcctg gctctgtaca accagcaciaa cccgggcgcg 240
 tcggcgggcg cgctgctgcgt gccgcaggcg ctggagccac tgcccatcgt gtactacgtg 300
 ggccgcaagc ccaaggtgga gcagctgtcc aacatgatcg tgcgttctg caagtgcagc 360
 tga 363

<210> 15
 <211> 120
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Porcine (Sus scrofa) TGF-beta1/FLAG (11/12) Fusion Construct

<220>
 <221> peptide
 <222> (12)..(19)
 <223> FLAG tag

<400> 15

Ala Leu Asp Thr Asn Tyr Cys Phe Ser Ser Thr Asp Tyr Lys Asp Asp
 1 5 10 15

Asp Asp Lys Glu Lys Asn Cys Cys Val Arg Gln Leu Tyr Ile Asp Phe

20

25

30

Arg Lys Asp Leu Gly Trp Lys Trp Ile His Glu Pro Lys Gly Tyr His
35 40 45

Ala Asn Phe Cys Leu Gly Pro Cys Pro Tyr Ile Trp Ser Leu Asp Thr
50 55 60

Gln Tyr Ser Lys Val Leu Ala Leu Tyr Asn Gln His Asn Pro Gly Ala
65 70 75 80

Ser Ala Ala Pro Cys Cys Val Pro Gln Ala Leu Glu Pro Leu Pro Ile
85 90 95

Val Tyr Tyr Val Gly Arg Lys Pro Lys Val Glu Gln Leu Ser Asn Met
100 105 110

Ile Val Arg Ser Cys Lys Cys Ser
115 120

<210> 16

<211> 1612

<212> DNA

<213> Artificial Sequence

<220>

<223> Murine (Mus musculus) TGF-beta1/N+5 FLAG Fusion Construct

<220>

<221> 5'UTR

<222> (1)..(347)

<223> 5' untranslated region

<220>

<221> CDS

<222> (348)..(1559)

<223> Protein coding sequence

<220>

<221> misc_feature

<222> (1182)..(1196)

<223> Encodes amino acid residues 1-5 of TGF-beta1

<220>

<221> misc_feature

<222> (1182)..(1159)

<223> Encodes mature fusion protein

<220>

<221> misc_feature
 <222> (1197)..(1220)
 <223> Encodes FLAG epitope tag

<220>
 <221> 3'UTR
 <222> (1560)..(1612)
 <223> 3' untranslated region

<400> 16
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 ctccctcgga cctgctggca gtagctcccc tatttaagaa caccacttt tggatctcag 120
 agagcgctca tctcgatttt taccttgggt gtatactgag acaccttggt gtcagagcct 180
 caccgcgact cctgctgctt tctccctcaa cctcaaatta ttcaggacta tcacctacct 240
 ttccttgga gacccacccc cacaagccct gcaggggcg ggccctcgca tcccaccttt 300
 gccgaggggt cccgctctcc gaagtgccgt ggggcgccgc ctcccc atg ccg ccc 356
 Met Pro Pro
 1
 tcg ggg ctg cgg cta ctg ccg ctt ctg ctc cca ctc ccg tgg ctt cta 404
 Ser Gly Leu Arg Leu Leu Pro Leu Leu Leu Pro Leu Pro Trp Leu Leu
 5 10 15
 gtg ctg acg ccc ggg agg cca gcc gcg gga ctc tcc acc tgc aag acc 452
 Val Leu Thr Pro Gly Arg Pro Ala Ala Gly Leu Ser Thr Cys Lys Thr
 20 25 30 35
 atc gac atg gag ctg gtg aaa cgg aag cgc atc gaa gcc atc cgt ggc 500
 Ile Asp Met Glu Leu Val Lys Arg Lys Arg Ile Glu Ala Ile Arg Gly
 40 45 50
 cag atc ctg tcc aaa cta agg ctc gcc agt ccc cca agc cag ggg gag 548
 Gln Ile Leu Ser Lys Leu Arg Leu Ala Ser Pro Pro Ser Gln Gly Glu
 55 60 65
 gta ccg ccc ggc ccg ctg ccc gag gcg gtg ctc gct ttg tac aac agc 596
 Val Pro Pro Gly Pro Leu Pro Glu Ala Val Leu Ala Leu Tyr Asn Ser
 70 75 80
 acc cgc gac cgg gtg gca ggc gag agc gcc gac cca gag ccg gag ccc 644
 Thr Arg Asp Arg Val Ala Gly Glu Ser Ala Asp Pro Glu Pro Glu Pro
 85 90 95
 gaa gcg gac tac tat gct aaa gag gtc acc cgc gtg cta atg gtg gac 692
 Glu Ala Asp Tyr Tyr Ala Lys Glu Val Thr Arg Val Leu Met Val Asp
 100 105 110 115
 cgc aac aac gcc atc tat gag aaa acc aaa gac atc tca cac agt ata 740
 Arg Asn Asn Ala Ile Tyr Glu Lys Thr Lys Asp Ile Ser His Ser Ile
 120 125 130
 tat atg ttc ttc aat acg tca gac att cgg gaa gca gtg ccc gaa ccc 788

Tyr Met Phe Phe Asn Thr Ser Asp Ile Arg Glu Ala Val Pro Glu Pro	
135 140 145	
cca ttg ctg tcc cgt gca gag ctg cgc ttg cag aga tta aaa tca agt	836
Pro Leu Leu Ser Arg Ala Glu Leu Arg Leu Gln Arg Leu Lys Ser Ser	
150 155 160	
gtg gag caa cat gtg gaa ctc tac cag aaa tat agc aac aat tcc tgg	884
Val Glu Gln His Val Glu Tyr Gln Lys Tyr Ser Asn Asn Ser Trp	
165 170 175	
cgt tac ctt ggt aac cgg ctg ctg acc ccc act gat acg cct gag tgg	932
Arg Tyr Leu Gly Asn Arg Leu Leu Thr Pro Thr Asp Thr Pro Glu Trp	
180 185 190 195	
ctg tct ttt gac gtc act gga gtt gta cgg cag tgg ctg aac caa gga	980
Leu Ser Phe Asp Val Thr Gly Val Val Arg Gln Trp Leu Asn Gln Gly	
200 205 210	
gac gga ata cag ggc ttt cga ttc agc gct cac tgc tct tgt gac agc	1028
Asp Gly Ile Gln Gly Phe Arg Phe Ser Ala His Cys Ser Cys Asp Ser	
215 220 225	
aaa gat aac aaa ctc cac gtg gaa atc aac ggg atc agc ccc aaa cgt	1076
Lys Asp Asn Lys Leu His Val Glu Ile Asn Gly Ile Ser Pro Lys Arg	
230 235 240	
cgg ggc gac ctg ggc acc atc cat gac atg aac cgg ccc ttc ctg ctc	1124
Arg Gly Asp Leu Gly Thr Ile His Asp Met Asn Arg Pro Phe Leu Leu	
245 250 255	
ctc atg gcc acc ccc ctg gaa agg gcc cag cac ctg cac agc tca cgg	1172
Leu Met Ala Thr Pro Leu Glu Arg Ala Gln His Leu His Ser Ser Arg	
260 265 270 275	
cac cgg aga gcc ctg gat acc aac gac tac aag gat gac gac gac aag	1220
His Arg Arg Ala Leu Asp Thr Asn Asp Tyr Lys Asp Asp Asp Asp Lys	
280 285 290	
gcc ctg gat acc aac tat tgc ttc agc tcc aca gag aag aac tgc tgt	1268
Ala Leu Asp Thr Asn Tyr Cys Phe Ser Ser Thr Glu Lys Asn Cys Cys	
295 300 305	
gtg cgg cag ctg tac att gac ttt agg aag gac ctg ggt tgg aag tgg	1316
Val Arg Gln Leu Tyr Ile Asp Phe Arg Lys Asp Leu Gly Trp Lys Trp	
310 315 320	
atc cac gag ccc aag ggc tac cat gcc aac ttc tgt ctg gga ccc tgc	1364
Ile His Glu Pro Lys Gly Tyr His Ala Asn Phe Cys Leu Gly Pro Cys	
325 330 335	
ccc tat att tgg agc ctg gac aca cag tac agc aag gtc ctt gcc ctc	1412
Pro Tyr Ile Trp Ser Leu Asp Thr Gln Tyr Ser Lys Val Leu Ala Leu	
340 345 350 355	
tac aac caa cac aac ccg ggc gct tcg gcg tca ccg tgc tgc gtg ccg	1460
Tyr Asn Gln His Asn Pro Gly Ala Ser Ala Ser Pro Cys Cys Val Pro	

Cl

360	365	370	
cag gct ttg gag cca ctg ccc atc gtc tac tac gtg ggt cgc aag ccc			1508
Gln Ala Leu Glu Pro Leu Pro Ile Val Tyr Tyr Val Gly Arg Lys Pro			
375	380	385	
aag gtg gag cag ttg tcc aac atg att gtg cgc tcc tgc aag tgc agc			1556
Lys Val Glu Gln Leu Ser Asn Met Ile Val Arg Ser Cys Lys Cys Ser			
390	395	400	
tga agccccgccc cgccccgccc ctcccggcag gcccggccccc gcccccgccc cgc			1612

<210> 17
 <211> 403
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Murine (Mus musculus) TGF-beta1/N+5 FLAG Fusion Construct

<400> 17

Met	Pro	Pro	Ser	Gly	Leu	Arg	Leu	Leu	Pro	Leu	Leu	Leu	Pro	Leu	Pro
1				5					10					15	

Trp	Leu	Leu	Val	Leu	Thr	Pro	Gly	Arg	Pro	Ala	Ala	Gly	Leu	Ser	Thr
			20					25					30		

Cys	Lys	Thr	Ile	Asp	Met	Glu	Leu	Val	Lys	Arg	Lys	Arg	Ile	Glu	Ala
			35				40					45			

Ile	Arg	Gly	Gln	Ile	Leu	Ser	Lys	Leu	Arg	Leu	Ala	Ser	Pro	Pro	Ser
	50					55					60				

Gln	Gly	Glu	Val	Pro	Pro	Gly	Pro	Leu	Pro	Glu	Ala	Val	Leu	Ala	Leu
65					70					75					80

Tyr	Asn	Ser	Thr	Arg	Asp	Arg	Val	Ala	Gly	Glu	Ser	Ala	Asp	Pro	Glu
				85					90					95	

Pro	Glu	Pro	Glu	Ala	Asp	Tyr	Tyr	Ala	Lys	Glu	Val	Thr	Arg	Val	Leu
			100					105					110		

Met	Val	Asp	Arg	Asn	Asn	Ala	Ile	Tyr	Glu	Lys	Thr	Lys	Asp	Ile	Ser
		115					120					125			

His	Ser	Ile	Tyr	Met	Phe	Phe	Asn	Thr	Ser	Asp	Ile	Arg	Glu	Ala	Val
	130					135					140				

Pro Glu Pro Pro Leu Leu Ser Arg Ala Glu Leu Arg Leu Gln Arg Leu
145 150 155 160

Lys Ser Ser Val Glu Gln His Val Glu Leu Tyr Gln Lys Tyr Ser Asn
165 170 175

Asn Ser Trp Arg Tyr Leu Gly Asn Arg Leu Leu Thr Pro Thr Asp Thr
180 185 190

Pro Glu Trp Leu Ser Phe Asp Val Thr Gly Val Val Arg Gln Trp Leu
195 200 205

Asn Gln Gly Asp Gly Ile Gln Gly Phe Arg Phe Ser Ala His Cys Ser
210 215 220

Cys Asp Ser Lys Asp Asn Lys Leu His Val Glu Ile Asn Gly Ile Ser
225 230 235 240

Pro Lys Arg Arg Gly Asp Leu Gly Thr Ile His Asp Met Asn Arg Pro
245 250 255

Phe Leu Leu Leu Met Ala Thr Pro Leu Glu Arg Ala Gln His Leu His
260 265 270

Ser Ser Arg His Arg Arg Ala Leu Asp Thr Asn Asp Tyr Lys Asp Asp
275 280 285

Asp Asp Lys Ala Leu Asp Thr Asn Tyr Cys Phe Ser Ser Thr Glu Lys
290 295 300

Asn Cys Cys Val Arg Gln Leu Tyr Ile Asp Phe Arg Lys Asp Leu Gly
305 310 315 320

Trp Lys Trp Ile His Glu Pro Lys Gly Tyr His Ala Asn Phe Cys Leu
325 330 335

Gly Pro Cys Pro Tyr Ile Trp Ser Leu Asp Thr Gln Tyr Ser Lys Val
340 345 350

Leu Ala Leu Tyr Asn Gln His Asn Pro Gly Ala Ser Ala Ser Pro Cys
355 360 365

Cys Val Pro Gln Ala Leu Glu Pro Leu Pro Ile Val Tyr Tyr Val Gly
 370 375 380

Arg Lys Pro Lys Val Glu Gln Leu Ser Asn Met Ile Val Arg Ser Cys
 385 390 395 400

Lys Cys Ser

<210> 18
 <211> 73
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer

<400> 18
 gccctggata ccaacgacta caaggatgac gacgacaagg ccctggatac caactactgc 60
 ttcagctcca cgg 73

<210> 19
 <211> 72
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer

<400> 19
 cttgtcgtcg tcacacctgt agtcgttatc cagggctcgg cggtggtgcc gggagctgtg 60
 caggtgctgg gc 72

<210> 20
 <211> 1624
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Murine (Mus musculus) TGF-beta1/N+5 HA Fusion Construct

<220>
 <221> 5'UTR
 <222> (1)..(347)
 <223> 5' untranslated region

<220>
 <221> CDS

<222> (348)..(1571)
 <223> Protein coding sequence

<220>
 <221> misc_feature
 <222> (1182)..(1196)
 <223> Encodes amino acid residues 1-5 of TGF-beta1

<220>
 <221> misc_feature
 <222> (1182)..(1571)
 <223> Encodes mature fusion protein

<220>
 <221> misc_feature
 <222> (1197)..(1232)
 <223> Encodes HA epitope tag

<220>
 <221> 3'UTR
 <222> (1572)..(1624)
 <223> 3' untranslated region

<400> 20
 cccagcctg cctcttgagt ccctcgcatc ccaggaccct ctctcccccg agaggcagat 60
 ctccctcgga cctgctggca gtagctcccc tatttaagaa caccacttt tggatctcag 120
 agagcgctca tctcgatttt taccctgggtg gtatactgag acaccttggt gtcagagcct 180
 caccgcgact cctgctgctt tctccctcaa cctcaaatta ttcaggacta tcacctacct 240
 ttccttgga gacccaccc cacaagccct gcaggggagg ggccctccgca tcccaccttt 300
 gccgagggtt cccgctctcc gaagtgccgt ggggagcgc ctcccc atg ccg ccc 356
 Met Pro Pro
 1
 tcg ggg ctg cgg cta ctg ccg ctt ctg ctc cca ctc ccg tgg ctt cta 404
 Ser Gly Leu Arg Leu Leu Pro Leu Leu Leu Pro Leu Pro Trp Leu Leu
 5 10 15
 gtg ctg acg ccc ggg agg cca gcc gcg gga ctc tcc acc tgc aag acc 452
 Val Leu Thr Pro Gly Arg Pro Ala Ala Gly Leu Ser Thr Cys Lys Thr
 20 25 30 35
 atc gac atg gag ctg gtg aaa cgg aag cgc atc gaa gcc atc cgt ggc 500
 Ile Asp Met Glu Leu Val Lys Arg Lys Arg Ile Glu Ala Ile Arg Gly
 40 45 50
 cag atc ctg tcc aaa cta agg ctc gcc agt ccc cca agc cag ggg gag 548
 Gln Ile Leu Ser Lys Leu Arg Leu Ala Ser Pro Pro Ser Gln Gly Glu
 55 60 65
 gta ccg ccc ggc ccg ctg ccc gag gcg gtg ctc gct ttg tac aac agc 596
 Val Pro Pro Gly Pro Leu Pro Glu Ala Val Leu Ala Leu Tyr Asn Ser
 70 75 80

acc cgc gac cgg gtg gca ggc gag agc gcc gac cca gag ccg gag ccc	644
Thr Arg Asp Arg Val Ala Gly Glu Ser Ala Asp Pro Glu Pro Glu Pro	
85 90 95	
 gaa gcg gac tac tat gct aaa gag gtc acc cgc gtg cta atg gtg gac	692
Glu Ala Asp Tyr Tyr Ala Lys Glu Val Thr Arg Val Leu Met Val Asp	
100 105 110 115	
 cgc aac aac gcc atc tat gag aaa acc aaa gac atc tca cac agt ata	740
Arg Asn Asn Ala Ile Tyr Glu Lys Thr Lys Asp Ile Ser His Ser Ile	
120 125 130	
 tat atg ttc ttc aat acg tca gac att cgg gaa gca gtg ccc gaa ccc	788
Tyr Met Phe Phe Asn Thr Ser Asp Ile Arg Glu Ala Val Pro Glu Pro	
135 140 145	
 cca ttg ctg tcc cgt gca gag ctg cgc ttg cag aga tta aaa tca agt	836
Pro Leu Leu Ser Arg Ala Glu Leu Arg Leu Gln Arg Leu Lys Ser Ser	
150 155 160	
 gtg gag caa cat gtg gaa ctc tac cag aaa tat agc aac aat tcc tgg	884
Val Glu Gln His Val Glu Leu Tyr Gln Lys Tyr Ser Asn Asn Ser Trp	
165 170 175	
 cgt tac ctt ggt aac cgg ctg ctg acc ccc act gat acg cct gag tgg	932
Arg Tyr Leu Gly Asn Arg Leu Leu Thr Pro Thr Asp Thr Pro Glu Trp	
180 185 190 195	
 ctg tct ttt gac gtc act gga gtt gta cgg cag tgg ctg aac caa gga	980
Leu Ser Phe Asp Val Thr Gly Val Val Arg Gln Trp Leu Asn Gln Gly	
200 205 210	
 gac gga ata cag ggc ttt cga ttc agc gct cac tgc tct tgt gac agc	1028
Asp Gly Ile Gln Gly Phe Arg Phe Ser Ala His Cys Ser Cys Asp Ser	
215 220 225	
 aaa gat aac aaa ctc cac gtg gaa atc aac ggg atc agc ccc aaa cgt	1076
Lys Asp Asn Lys Leu His Val Glu Ile Asn Gly Ile Ser Pro Lys Arg	
230 235 240	
 cgg ggc gac ctg ggc acc atc cat gac atg aac cgg ccc ttc ctg ctc	1124
Arg Gly Asp Leu Gly Thr Ile His Asp Met Asn Arg Pro Phe Leu Leu	
245 250 255	
 ctc atg gcc acc ccc ctg gaa agg gcc cag cac ctg cac agc tca cgg	1172
Leu Met Ala Thr Pro Leu Glu Arg Ala Gln His Leu His Ser Ser Arg	
260 265 270 275	
 cac cgg aga gcc ctg gat acc aac agc tac cca tac gac gtg cca gac	1220
His Arg Arg Ala Leu Asp Thr Asn Ser Tyr Pro Tyr Asp Val Pro Asp	
280 285 290	
 tac gca tct ctg gcc ctg gat acc aac tat tgc ttc agc tcc aca gag	1268
Tyr Ala Ser Leu Ala Leu Asp Thr Asn Tyr Cys Phe Ser Ser Thr Glu	
295 300 305	

aag aac tgc tgt gtg cgg cag ctg tac att gac ttt agg aag gac ctg 1316
 Lys Asn Cys Cys Val Arg Gln Leu Tyr Ile Asp Phe Arg Lys Asp Leu
 310 315 320

ggg tgg aag tgg atc cac gag ccc aag ggc tac cat gcc aac ttc tgt 1364
 Gly Trp Lys Trp Ile His Glu Pro Lys Gly Tyr His Ala Asn Phe Cys
 325 330 335

ctg gga ccc tgc ccc tat att tgg agc ctg gac aca cag tac agc aag 1412
 Leu Gly Pro Cys Pro Tyr Ile Trp Ser Leu Asp Thr Gln Tyr Ser Lys
 340 345 350 355

gtc ctt gcc ctc tac aac caa cac aac ccg ggc gct tcg gcg tca ccg 1460
 Val Leu Ala Leu Tyr Asn Gln His Asn Pro Gly Ala Ser Ala Ser Pro
 360 365 370

tgc tgc gtg ccg cag gct ttg gag cca ctg ccc atc gtc tac tac gtg 1508
 Cys Cys Val Pro Gln Ala Leu Glu Pro Leu Pro Ile Val Tyr Tyr Val
 375 380 385

ggg cgc aag ccc aag gtg gag cag ttg tcc aac atg att gtg cgc tcc 1556
 Gly Arg Lys Pro Lys Val Glu Gln Leu Ser Asn Met Ile Val Arg Ser
 390 395 400

tgc aag tgc agc tga agccccgccc cgccccgccc ctcccggcag gcccgcccc 1611
 Cys Lys Cys Ser
 405

gcccccgccc cgc 1624

<210> 21
 <211> 407
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Murine (Mus musculus) TGF-beta1/N+5 HA Fusion Construct

<400> 21

Met Pro Pro Ser Gly Leu Arg Leu Leu Pro Leu Leu Leu Pro Leu Pro
 1 5 10 15

Trp Leu Leu Val Leu Thr Pro Gly Arg Pro Ala Ala Gly Leu Ser Thr
 20 25 30

Cys Lys Thr Ile Asp Met Glu Leu Val Lys Arg Lys Arg Ile Glu Ala
 35 40 45

Ile Arg Gly Gln Ile Leu Ser Lys Leu Arg Leu Ala Ser Pro Pro Ser
 50 55 60

Gln Gly Glu Val Pro Pro Gly Pro Leu Pro Glu Ala Val Leu Ala Leu
65 70 75 80

Tyr Asn Ser Thr Arg Asp Arg Val Ala Gly Glu Ser Ala Asp Pro Glu
85 90 95

Pro Glu Pro Glu Ala Asp Tyr Tyr Ala Lys Glu Val Thr Arg Val Leu
100 105 110

Met Val Asp Arg Asn Asn Ala Ile Tyr Glu Lys Thr Lys Asp Ile Ser
115 120 125

His Ser Ile Tyr Met Phe Phe Asn Thr Ser Asp Ile Arg Glu Ala Val
130 135 140

Pro Glu Pro Pro Leu Leu Ser Arg Ala Glu Leu Arg Leu Gln Arg Leu
145 150 155 160

Lys Ser Ser Val Glu Gln His Val Glu Leu Tyr Gln Lys Tyr Ser Asn
165 170 175

Asn Ser Trp Arg Tyr Leu Gly Asn Arg Leu Leu Thr Pro Thr Asp Thr
180 185 190

Pro Glu Trp Leu Ser Phe Asp Val Thr Gly Val Val Arg Gln Trp Leu
195 200 205

Asn Gln Gly Asp Gly Ile Gln Gly Phe Arg Phe Ser Ala His Cys Ser
210 215 220

Cys Asp Ser Lys Asp Asn Lys Leu His Val Glu Ile Asn Gly Ile Ser
225 230 235 240

Pro Lys Arg Arg Gly Asp Leu Gly Thr Ile His Asp Met Asn Arg Pro
245 250 255

Phe Leu Leu Leu Met Ala Thr Pro Leu Glu Arg Ala Gln His Leu His
260 265 270

Ser Ser Arg His Arg Arg Ala Leu Asp Thr Asn Ser Tyr Pro Tyr Asp
275 280 285

Val Pro Asp Tyr Ala Ser Leu Ala Leu Asp Thr Asn Tyr Cys Phe Ser

290

295

300

Ser Thr Glu Lys Asn Cys Cys Val Arg Gln Leu Tyr Ile Asp Phe Arg
305 310 315 320

Lys Asp Leu Gly Trp Lys Trp Ile His Glu Pro Lys Gly Tyr His Ala
325 330 335

Asn Phe Cys Leu Gly Pro Cys Pro Tyr Ile Trp Ser Leu Asp Thr Gln
340 345 350

Tyr Ser Lys Val Leu Ala Leu Tyr Asn Gln His Asn Pro Gly Ala Ser
355 360 365

Ala Ser Pro Cys Cys Val Pro Gln Ala Leu Glu Pro Leu Pro Ile Val
370 375 380

Tyr Tyr Val Gly Arg Lys Pro Lys Val Glu Gln Leu Ser Asn Met Ile
385 390 395 400

Val Arg Ser Cys Lys Cys Ser
405

<210> 22
<211> 108
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 22
gccctggata ccaacagcta cccatacgac gtgccagact acgcatctct ggccctggat 60
accaactact gcttcagctc cacggagaag aactgctgcg tgcggcag 108

<210> 23
<211> 73
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 23
cagagatgcg tagtctggca cgtcgtatgg gtagctgttg gtatccaggg ctcggcggtg 60
ccgggagctg tgc 73

<210> 24
 <211> 1284
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Murine (Mus musculus) TGF-beta2/N+5 FLAG Fusion Construct

<220>
 <221> CDS
 <222> (1)..(1284)
 <223> Protein coding sequence

<220>
 <221> misc_feature
 <222> (907)..(921)
 <223> Encodes amino acid residues 1-5 of TGF-beta2

<220>
 <221> misc_feature
 <222> (907)..(1284)
 <223> Encodes mature fusion protein

<220>
 <221> misc_feature
 <222> (922)..(945)
 <223> Encodes FLAG epitope tag

<400> 24
 atg cac tac tgt gtg ctg agc acc ttt ttg ctc ctg cat ctg gtc ccg 48
 Met His Tyr Cys Val Leu Ser Thr Phe Leu Leu Leu His Leu Val Pro
 1 5 10 15

gtg gcg ctc agt ctg tct acc tgc agc acc ctc gac atg gat cag ttt 96
 Val Ala Leu Ser Leu Ser Thr Cys Ser Thr Leu Asp Met Asp Gln Phe
 20 25 30

atg cgc aag agg atc gag gcc atc cgc ggg cag atc ctg agc aag ctg 144
 Met Arg Lys Arg Ile Glu Ala Ile Arg Gly Gln Ile Leu Ser Lys Leu
 35 40 45

aag ctc acc agc ccc ccg gaa gac tat ccg gag ccg gat gag gtc ccc 192
 Lys Leu Thr Ser Pro Pro Glu Asp Tyr Pro Glu Pro Asp Glu Val Pro
 50 55 60

ccg gag gtg att tcc atc tac aac agt acc agg gac tta ctg cag gag 240
 Pro Glu Val Ile Ser Ile Tyr Asn Ser Thr Arg Asp Leu Leu Gln Glu
 65 70 75 80

aag gca agc cgg agg gca gcc gcc tgc gag cgc gag cgg agc gag cag 288
 Lys Ala Ser Arg Arg Ala Ala Ala Cys Glu Arg Glu Arg Ser Glu Gln
 85 90 95

gag tac tac gcc aag gag gtt tat aaa atc gac atg ccg tcc cac ctc 336

Glu Tyr Tyr Ala Lys Glu Val Tyr Lys Ile Asp Met Pro Ser His Leu	
100	105 110
ccc tcc gaa aat gcc atc ccg ccc act ttc tac aga ccc tac ttc aga	384
Pro Ser Glu Asn Ala Ile Pro Pro Thr Phe Tyr Arg Pro Tyr Phe Arg	
115	120 125
atc gtc cgc ttt gat gtc tca aca atg gag aaa aat gct tcg aat ctg	432
Ile Val Arg Phe Asp Val Ser Thr Met Glu Lys Asn Ala Ser Asn Leu	
130	135 140
gtg aag gca gag ttc agg gtc ttc cgc ttg caa aac ccc aaa gcc aga	480
Val Lys Ala Glu Phe Arg Val Phe Arg Leu Gln Asn Pro Lys Ala Arg	
145	150 155 160
gtg gcc gag cag cgg att gaa ctg tat cag atc ctt aaa tcc aaa gac	528
Val Ala Glu Gln Arg Ile Glu Leu Tyr Gln Ile Leu Lys Ser Lys Asp	
165	170 175
tta aca tct ccc acc cag cgc tac atc gat agc aag gtt gtg aaa acc	576
Leu Thr Ser Pro Thr Gln Arg Tyr Ile Asp Ser Lys Val Val Lys Thr	
180	185 190
aga gcg gag ggt gaa tgg ctc tcc ttc gac gtg aca gac gct gtg cag	624
Arg Ala Glu Gly Glu Trp Leu Ser Phe Asp Val Thr Asp Ala Val Gln	
195	200 205
gag tgg ctt cac cac aaa gac agg aac ctg ggg ttt aaa ata agt tta	672
Glu Trp Leu His His Lys Asp Arg Asn Leu Gly Phe Lys Ile Ser Leu	
210	215 220
cac tgc ccc tgc tgt acc ttc gtg ccg tct aat aat tac atc atc ccg	720
His Cys Pro Cys Cys Thr Phe Val Pro Ser Asn Asn Tyr Ile Ile Pro	
225	230 235 240
aat aaa agc gaa gag ctc gag gcg aga ttt gca ggt att gat ggc acc	768
Asn Lys Ser Glu Glu Leu Glu Ala Arg Phe Ala Gly Ile Asp Gly Thr	
245	250 255
tct aca tat gcc agt ggt gat cag aaa act ata aag tcc act agg aaa	816
Ser Thr Tyr Ala Ser Gly Asp Gln Lys Thr Ile Lys Ser Thr Arg Lys	
260	265 270
aaa acc agt ggg aag acc cca cat ctc ctg cta atg ttg ttg ccc tcc	864
Lys Thr Ser Gly Lys Thr Pro His Leu Leu Leu Met Leu Leu Pro Ser	
275	280 285
tac aga ctg gag tca caa cag tcc agc cgg cgg aag aag cgc gct ttg	912
Tyr Arg Leu Glu Ser Gln Gln Ser Ser Arg Arg Lys Lys Arg Ala Leu	
290	295 300
gat gct gcc gac tac aag gat gac gac gac aag gct ttg gat gct gcc	960
Asp Ala Ala Asp Tyr Lys Asp Asp Asp Asp Lys Ala Leu Asp Ala Ala	
305	310 315 320
tac tgc ttt aga aat gtg cag gat aat tgc tgc ctt cgc cct ctt tac	1008
Tyr Cys Phe Arg Asn Val Gln Asp Asn Cys Cys Leu Arg Pro Leu Tyr	

325	330	335	
att gat ttt aag agg gat ctt gga tgg aaa tgg atc cat gaa ccc aaa			1056
Ile Asp Phe Lys Arg Asp Leu Gly Trp Lys Trp Ile His Glu Pro Lys			
340	345	350	
ggg tac aat gct aac ttc tgt gct ggg gca tgc cca tat cta tgg agt			1104
Gly Tyr Asn Ala Asn Phe Cys Ala Gly Ala Cys Pro Tyr Leu Trp Ser			
355	360	365	
tca gac act caa cac acc aaa gtc ctc agc ctg tac aac acc ata aat			1152
Ser Asp Thr Gln His Thr Lys Val Leu Ser Leu Tyr Asn Thr Ile Asn			
370	375	380	
ccc gaa gct tcc gct tcc cct tgc tgt gtg tcc cag gat ctg gaa cca			1200
Pro Glu Ala Ser Ala Ser Pro Cys Cys Val Ser Gln Asp Leu Glu Pro			
385	390	395	400
ctg acc att ctc tat tac att gga aat acg ccc aag atc gaa cag ctt			1248
Leu Thr Ile Leu Tyr Tyr Ile Gly Asn Thr Pro Lys Ile Glu Gln Leu			
405	410	415	
tcc aat atg att gtc aag tct tgt aaa tgc agc taa			1284
Ser Asn Met Ile Val Lys Ser Cys Lys Cys Ser			
420	425		

C1

<210> 25
 <211> 427
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Murine (Mus musculus) TGF-beta2/N+5 FLAG Fusion Construct

<400> 25

Met His Tyr Cys Val Leu Ser Thr Phe Leu Leu Leu His Leu Val Pro
 1 5 10 15

Val Ala Leu Ser Leu Ser Thr Cys Ser Thr Leu Asp Met Asp Gln Phe
 20 25 30

Met Arg Lys Arg Ile Glu Ala Ile Arg Gly Gln Ile Leu Ser Lys Leu
 35 40 45

Lys Leu Thr Ser Pro Pro Glu Asp Tyr Pro Glu Pro Asp Glu Val Pro
 50 55 60

Pro Glu Val Ile Ser Ile Tyr Asn Ser Thr Arg Asp Leu Leu Gln Glu
 65 70 75 80

Lys Ala Ser Arg Arg Ala Ala Ala Cys Glu Arg Glu Arg Ser Glu Gln
85 90 95

Glu Tyr Tyr Ala Lys Glu Val Tyr Lys Ile Asp Met Pro Ser His Leu
100 105 110

Pro Ser Glu Asn Ala Ile Pro Pro Thr Phe Tyr Arg Pro Tyr Phe Arg
115 120 125

Ile Val Arg Phe Asp Val Ser Thr Met Glu Lys Asn Ala Ser Asn Leu
130 135 140

Val Lys Ala Glu Phe Arg Val Phe Arg Leu Gln Asn Pro Lys Ala Arg
145 150 155 160

Val Ala Glu Gln Arg Ile Glu Leu Tyr Gln Ile Leu Lys Ser Lys Asp
165 170 175

Leu Thr Ser Pro Thr Gln Arg Tyr Ile Asp Ser Lys Val Val Lys Thr
180 185 190

CI Arg Ala Glu Gly Glu Trp Leu Ser Phe Asp Val Thr Asp Ala Val Gln
195 200 205

Glu Trp Leu His His Lys Asp Arg Asn Leu Gly Phe Lys Ile Ser Leu
210 215 220

His Cys Pro Cys Cys Thr Phe Val Pro Ser Asn Asn Tyr Ile Ile Pro
225 230 235 240

Asn Lys Ser Glu Glu Leu Glu Ala Arg Phe Ala Gly Ile Asp Gly Thr
245 250 255

Ser Thr Tyr Ala Ser Gly Asp Gln Lys Thr Ile Lys Ser Thr Arg Lys
260 265 270

Lys Thr Ser Gly Lys Thr Pro His Leu Leu Leu Met Leu Leu Pro Ser
275 280 285

Tyr Arg Leu Glu Ser Gln Gln Ser Ser Arg Arg Lys Lys Arg Ala Leu
290 295 300

Asp Ala Ala Asp Tyr Lys Asp Asp Asp Asp Lys Ala Leu Asp Ala Ala

305 310 315 320

Tyr Cys Phe Arg Asn Val Gln Asp Asn Cys Cys Leu Arg Pro Leu Tyr
325 330 335

Ile Asp Phe Lys Arg Asp Leu Gly Trp Lys Trp Ile His Glu Pro Lys
340 345 350

Gly Tyr Asn Ala Asn Phe Cys Ala Gly Ala Cys Pro Tyr Leu Trp Ser
355 360 365

Ser Asp Thr Gln His Thr Lys Val Leu Ser Leu Tyr Asn Thr Ile Asn
370 375 380

Pro Glu Ala Ser Ala Ser Pro Cys Cys Val Ser Gln Asp Leu Glu Pro
385 390 395 400

Leu Thr Ile Leu Tyr Tyr Ile Gly Asn Thr Pro Lys Ile Glu Gln Leu
405 410 415

Ser Asn Met Ile Val Lys Ser Cys Lys Cys Ser
420 425

C1

<210> 26
<211> 1303
<212> DNA
<213> Artificial Sequence

<220>
<223> Murine (Mus musculus) TGF-beta2/N+5 HA Fusion Construct

<220>
<221> 5'UTR
<222> (1)..(7)
<223> 5' untranslated region

<220>
<221> CDS
<222> (8)..(1303)
<223> Protein coding sequence

<220>
<221> misc_feature
<222> (914)..(928)
<223> Encodes amino acid residues 1-5 of TGF-beta2

<220>
<221> misc_feature

<222> (914)..(1303)
 <223> Encodes mature fusion protein

<220>
 <221> misc_feature
 <222> (929)..(964)
 <223> Encodes HA epitope tag

<400> 26
 taaaaaac atg cac tac tgt gtg ctg agc acc ttt ttg ctc ctg cat ctg 49
 Met His Tyr Cys Val Leu Ser Thr Phe Leu Leu Leu His Leu
 1 5 10

gtc ccg gtg gcg ctc agt ctg tct acc tgc agc acc ctc gac atg gat 97
 Val Pro Val Ala Leu Ser Leu Ser Thr Cys Ser Thr Leu Asp Met Asp
 15 20 25 30

cag ttt atg cgc aag agg atc gag gcc atc cgc ggg cag atc ctg agc 145
 Gln Phe Met Arg Lys Arg Ile Glu Ala Ile Arg Gly Gln Ile Leu Ser
 35 40 45

aag ctg aag ctc acc agc ccc ccg gaa gac tat ccg gag ccg gat gag 193
 Lys Leu Lys Leu Thr Ser Pro Pro Glu Asp Tyr Pro Glu Pro Asp Glu
 50 55 60

gtc ccc ccg gag gtg att tcc atc tac aac agt acc agg gac tta ctg 241
 Val Pro Pro Glu Val Ile Ser Ile Tyr Asn Ser Thr Arg Asp Leu Leu
 65 70 75

cag gag aag gca agc cgg agg gca gcc gcc tgc gag cgc gag cgg agc 289
 Gln Glu Lys Ala Ser Arg Arg Ala Ala Ala Cys Glu Arg Glu Arg Ser
 80 85 90

gag cag gag tac tac gcc aag gag gtt tat aaa atc gac atg ccg tcc 337
 Glu Gln Glu Tyr Tyr Ala Lys Glu Val Tyr Lys Ile Asp Met Pro Ser
 95 100 105 110

cac ctc ccc tcc gaa aat gcc atc ccg ccc act ttc tac aga ccc tac 385
 His Leu Pro Ser Glu Asn Ala Ile Pro Pro Thr Phe Tyr Arg Pro Tyr
 115 120 125

ttc aga atc gtc cgc ttt gat gtc tca aca atg gag aaa aat gct tcg 433
 Phe Arg Ile Val Arg Phe Asp Val Ser Thr Met Glu Lys Asn Ala Ser
 130 135 140

aat ctg gtg aag gca gag ttc agg gtc ttc cgc ttg caa aac ccc aaa 481
 Asn Leu Val Lys Ala Glu Phe Arg Val Phe Arg Leu Gln Asn Pro Lys
 145 150 155

gcc aga gtg gcc gag cag cgg att gaa ctg tat cag atc ctt aaa tcc 529
 Ala Arg Val Ala Glu Gln Arg Ile Glu Leu Tyr Gln Ile Leu Lys Ser
 160 165 170

aaa gac tta aca tct ccc acc cag cgc tac atc gat agc aag gtt gtg 577
 Lys Asp Leu Thr Ser Pro Thr Gln Arg Tyr Ile Asp Ser Lys Val Val
 175 180 185 190

C1

aaa acc aga gcg gag ggt gaa tgg ctc tcc ttc gac gtg aca gac gct	625
Lys Thr Arg Ala Glu Gly Glu Trp Leu Ser Phe Asp Val Thr Asp Ala	
195 200 205	
gtg cag gag tgg ctt cac cac aaa gac agg aac ctg ggg ttt aaa ata	673
Val Gln Glu Trp Leu His His Lys Asp Arg Asn Leu Gly Phe Lys Ile	
210 215 220	
agt tta cac tgc ccc tgc tgt acc ttc gtg ccg tct aat aat tac atc	721
Ser Leu His Cys Pro Cys Cys Thr Phe Val Pro Ser Asn Asn Tyr Ile	
225 230 235	
atc ccg aat aaa agc gaa gag ctc gag gcg aga ttt gca ggt att gat	769
Ile Pro Asn Lys Ser Glu Glu Leu Glu Ala Arg Phe Ala Gly Ile Asp	
240 245 250	
ggc acc tct aca tat gcc agt ggt gat cag aaa act ata aag tcc act	817
Gly Thr Ser Thr Tyr Ala Ser Gly Asp Gln Lys Thr Ile Lys Ser Thr	
255 260 265 270	
agg aaa aaa acc agt ggg aag acc cca cat ctc ctg cta atg ttg ttg	865
Arg Lys Lys Thr Ser Gly Lys Thr Pro His Leu Leu Leu Met Leu Leu	
275 280 285	
ccc tcc tac aga ctg gag tca caa cag tcc agc cgg cgg aag aag cgc	913
Pro Ser Tyr Arg Leu Glu Ser Gln Gln Ser Ser Arg Arg Lys Lys Arg	
290 295 300	
CI gct ttg gat gct gcc agc tac cca tac gac gtg cca gac tac gca tct	961
Ala Leu Asp Ala Ala Ser Tyr Pro Tyr Asp Val Pro Asp Tyr Ala Ser	
305 310 315	
ctg gct ttg gat gct gcc tac tgc ttt aga aat gtg cag gat aat tgc	1009
Leu Ala Leu Asp Ala Ala Tyr Cys Phe Arg Asn Val Gln Asp Asn Cys	
320 325 330	
tgc ctt cgc cct ctt tac att gat ttt aag agg gat ctt gga tgg aaa	1057
Cys Leu Arg Pro Leu Tyr Ile Asp Phe Lys Arg Asp Leu Gly Trp Lys	
335 340 345 350	
tgg atc cat gaa ccc aaa ggg tac aat gct aac ttc tgt gct ggg gca	1105
Trp Ile His Glu Pro Lys Gly Tyr Asn Ala Asn Phe Cys Ala Gly Ala	
355 360 365	
tgc cca tat cta tgg agt tca gac act caa cac acc aaa gtc ctc agc	1153
Cys Pro Tyr Leu Trp Ser Ser Asp Thr Gln His Thr Lys Val Leu Ser	
370 375 380	
ctg tac aac acc ata aat ccc gaa gct tcc gct tcc cct tgc tgt gtg	1201
Leu Tyr Asn Thr Ile Asn Pro Glu Ala Ser Ala Ser Pro Cys Cys Val	
385 390 395	
tcc cag gat ctg gaa cca ctg acc att ctc tat tac att gga aat acg	1249
Ser Gln Asp Leu Glu Pro Leu Thr Ile Leu Tyr Tyr Ile Gly Asn Thr	
400 405 410	
ccc aag atc gaa cag ctt tcc aat atg att gtc aag tct tgt aaa tgc	1297

Pro Lys Ile Glu Gln Leu Ser Asn Met Ile Val Lys Ser Cys Lys Cys
 415 420 425 430

agc taa
 Ser

1303

<210> 27
 <211> 431
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Murine (Mus musculus) TGF-beta2/N+5 HA Fusion Construct

<400> 27

Met His Tyr Cys Val Leu Ser Thr Phe Leu Leu Leu His Leu Val Pro
 1 5 10 15

Val Ala Leu Ser Leu Ser Thr Cys Ser Thr Leu Asp Met Asp Gln Phe
 20 25 30

Met Arg Lys Arg Ile Glu Ala Ile Arg Gly Gln Ile Leu Ser Lys Leu
 35 40 45

Lys Leu Thr Ser Pro Pro Glu Asp Tyr Pro Glu Pro Asp Glu Val Pro
 50 55 60

Pro Glu Val Ile Ser Ile Tyr Asn Ser Thr Arg Asp Leu Leu Gln Glu
 65 70 75 80

Lys Ala Ser Arg Arg Ala Ala Ala Cys Glu Arg Glu Arg Ser Glu Gln
 85 90 95

Glu Tyr Tyr Ala Lys Glu Val Tyr Lys Ile Asp Met Pro Ser His Leu
 100 105 110

Pro Ser Glu Asn Ala Ile Pro Pro Thr Phe Tyr Arg Pro Tyr Phe Arg
 115 120 125

Ile Val Arg Phe Asp Val Ser Thr Met Glu Lys Asn Ala Ser Asn Leu
 130 135 140

Val Lys Ala Glu Phe Arg Val Phe Arg Leu Gln Asn Pro Lys Ala Arg
 145 150 155 160

Val Ala Glu Gln Arg Ile Glu Leu Tyr Gln Ile Leu Lys Ser Lys Asp
165 170 175

Leu Thr Ser Pro Thr Gln Arg Tyr Ile Asp Ser Lys Val Val Lys Thr
180 185 190

Arg Ala Glu Gly Glu Trp Leu Ser Phe Asp Val Thr Asp Ala Val Gln
195 200 205

Glu Trp Leu His His Lys Asp Arg Asn Leu Gly Phe Lys Ile Ser Leu
210 215 220

His Cys Pro Cys Cys Thr Phe Val Pro Ser Asn Asn Tyr Ile Ile Pro
225 230 235 240

Asn Lys Ser Glu Glu Leu Glu Ala Arg Phe Ala Gly Ile Asp Gly Thr
245 250 255

Ser Thr Tyr Ala Ser Gly Asp Gln Lys Thr Ile Lys Ser Thr Arg Lys
260 265 270

CI Lys Thr Ser Gly Lys Thr Pro His Leu Leu Leu Met Leu Leu Pro Ser
275 280 285

Tyr Arg Leu Glu Ser Gln Gln Ser Ser Arg Arg Lys Lys Arg Ala Leu
290 295 300

Asp Ala Ala Ser Tyr Pro Tyr Asp Val Pro Asp Tyr Ala Ser Leu Ala
305 310 315 320

Leu Asp Ala Ala Tyr Cys Phe Arg Asn Val Gln Asp Asn Cys Cys Leu
325 330 335

Arg Pro Leu Tyr Ile Asp Phe Lys Arg Asp Leu Gly Trp Lys Trp Ile
340 345 350

His Glu Pro Lys Gly Tyr Asn Ala Asn Phe Cys Ala Gly Ala Cys Pro
355 360 365

Tyr Leu Trp Ser Ser Asp Thr Gln His Thr Lys Val Leu Ser Leu Tyr
370 375 380

Asn Thr Ile Asn Pro Glu Ala Ser Ala Ser Pro Cys Cys Val Ser Gln
385 390 395 400

Asp Leu Glu Pro Leu Thr Ile Leu Tyr Tyr Ile Gly Asn Thr Pro Lys
405 410 415

Ile Glu Gln Leu Ser Asn Met Ile Val Lys Ser Cys Lys Cys Ser
420 425 430

<210> 28
<211> 1272
<212> DNA
<213> Artificial Sequence

<220>
<223> Murine (Mus musculus) TGF-beta3/N+5 FLAG Fusion Construct

<220>
<221> CDS
<222> (1)..(1272)
<223> Protein coding sequence

<220>
<221> misc_feature
<222> (895)..(909)
<223> Encodes amino acid residues 1-5 of TGF-beta3

<220>
<221> misc_feature
<222> (895)..(1272)
<223> Encodes mature fusion protein

<220>
<221> misc_feature
<222> (910)..(933)
<223> Encodes FLAG epitope tag

<400> 28
atg cac ttg caa agg gct ctg gta gtc ctg gcc ctg ctg aac ttg gcc 48
Met His Leu Gln Arg Ala Leu Val Val Leu Ala Leu Leu Asn Leu Ala
1 5 10 15

aca atc agc ctc tct ctg tcc act tgc acc acg ttg gac ttc ggc cac 96
Thr Ile Ser Leu Ser Leu Ser Thr Cys Thr Thr Leu Asp Phe Gly His
20 25 30

atc aag aag aag agg gtg gaa gcc att agg gga cag atc ttg agc aag 144
Ile Lys Lys Lys Arg Val Glu Ala Ile Arg Gly Gln Ile Leu Ser Lys
35 40 45

ctc agg ctc acc agc ccc cct gag cca tgc gtg atg acc cac gtc ccc 192
Leu Arg Leu Thr Ser Pro Pro Glu Pro Ser Val Met Thr His Val Pro
50 55 60

tat cag gtc ctg gca ctt tac aac agc acc cgg gag ttg ctg gaa gag	240
Tyr Gln Val Leu Ala Leu Tyr Asn Ser Thr Arg Glu Leu Leu Glu Glu	
65 70 75 80	
atg cac ggg gag agg gag gaa ggc tgc act cag gag acc tcg gag tct	288
Met His Gly Glu Arg Glu Glu Gly Cys Thr Gln Glu Thr Ser Glu Ser	
85 90 95	
gag tac tat gcc aaa gag atc cat aaa ttc gac atg atc cag gga ctg	336
Glu Tyr Tyr Ala Lys Glu Ile His Lys Phe Asp Met Ile Gln Gly Leu	
100 105 110	
gcg gag cac aat gaa ctg gcc gtc tgc ccc aaa gga att acc tct aag	384
Ala Glu His Asn Glu Leu Ala Val Cys Pro Lys Gly Ile Thr Ser Lys	
115 120 125	
gtt ttt cgt ttc aat gtg tcc tca gtg gag aaa aat gga acc aat ctg	432
Val Phe Arg Phe Asn Val Ser Ser Val Glu Lys Asn Gly Thr Asn Leu	
130 135 140	
ttc cgg gca gag ttc cgg gtc ttg cgg gtg ccc aac ccc agc tcc aag	480
Phe Arg Ala Glu Phe Arg Val Leu Arg Val Pro Asn Pro Ser Ser Lys	
145 150 155 160	
cgc aca gag cag aga att gag ctc ttc cag ata ctt cga ccg gat gag	528
Arg Thr Glu Gln Arg Ile Glu Leu Phe Gln Ile Leu Arg Pro Asp Glu	
165 170 175	
cac ata gcc aag cag cgc tac ata ggt ggc aag aat ctg ccc aca agg	576
His Ile Ala Lys Gln Arg Tyr Ile Gly Gly Lys Asn Leu Pro Thr Arg	
180 185 190	
ggc acc gct gaa tgg ctg tct ttc gat gtc act gac act gtg cgc gag	624
Gly Thr Ala Glu Trp Leu Ser Phe Asp Val Thr Asp Thr Val Arg Glu	
195 200 205	
tgg ctg ttg agg aga gag tcc aac ttg ggt ctg gaa atc agc atc cac	672
Trp Leu Leu Arg Arg Glu Ser Asn Leu Gly Leu Glu Ile Ser Ile His	
210 215 220	
tgt cca tgt cac acc ttt cag ccc aat gga gac ata ctg gaa aat gtt	720
Cys Pro Cys His Thr Phe Gln Pro Asn Gly Asp Ile Leu Glu Asn Val	
225 230 235 240	
cat gag gtg atg gaa atc aaa ttc aaa gga gtg gac aat gaa gat gac	768
His Glu Val Met Glu Ile Lys Phe Lys Gly Val Asp Asn Glu Asp Asp	
245 250 255	
cat ggc cgt gga gac ctg ggg cgt ctc aag aag caa aag gat cac cac	816
His Gly Arg Gly Asp Leu Gly Arg Leu Lys Lys Gln Lys Asp His His	
260 265 270	
aac cca cac ctg atc ctc atg atg atc ccc cca cac cga ctg gac agc	864
Asn Pro His Leu Ile Leu Met Met Ile Pro Pro His Arg Leu Asp Ser	
275 280 285	

C1

cca ggc cag ggc agt cag agg aag aag agg gcc ctg gac acc aat gac 912
 Pro Gly Gln Gly Ser Gln Arg Lys Lys Arg Ala Leu Asp Thr Asn Asp
 290 295 300

tac aag gat gac gac gac aag gcc ctg gac acc aat tac tgc ttc cgc 960
 Tyr Lys Asp Asp Asp Lys Ala Leu Asp Thr Asn Tyr Cys Phe Arg
 305 310 315 320

aac ctg gag gag aac tgc tgt gta cgc ccc ctt tat att gac ttc cgg 1008
 Asn Leu Glu Glu Asn Cys Cys Val Arg Pro Leu Tyr Ile Asp Phe Arg
 325 330 335

cag gat cta ggc tgg aaa tgg gtc cac gaa cct aag ggt tac tat gcc 1056
 Gln Asp Leu Gly Trp Lys Trp Val His Glu Pro Lys Gly Tyr Tyr Ala
 340 345 350

aac ttc tgc tca ggc cct tgc cca tac ctc cgc agc gca gac aca acc 1104
 Asn Phe Cys Ser Gly Pro Cys Pro Tyr Leu Arg Ser Ala Asp Thr Thr
 355 360 365

cat agc acg gtg ctt gga cta tac aac acc ctg aac cca gag gcg tct 1152
 His Ser Thr Val Leu Gly Leu Tyr Asn Thr Leu Asn Pro Glu Ala Ser
 370 375 380

gcc tcg cca tgc tgc gtc ccc cag gac ctg gag ccc ctg acc atc ttg 1200
 Ala Ser Pro Cys Cys Val Pro Gln Asp Leu Glu Pro Leu Thr Ile Leu
 385 390 395 400

CI tac tat gtg ggc aga acc ccc aag gtg gag cag ctg tcc aac atg gtg 1248
 Tyr Tyr Val Gly Arg Thr Pro Lys Val Glu Gln Leu Ser Asn Met Val
 405 410 415

gtg aag tcg tgt aag tgc agc tga 1272
 Val Lys Ser Cys Lys Cys Ser
 420

<210> 29

<211> 423

<212> PRT

<213> Artificial Sequence

<220>

<223> Murine (Mus musculus) TGF-beta3/N+5 FLAG Fusion Construct

<400> 29

Met His Leu Gln Arg Ala Leu Val Val Leu Ala Leu Leu Asn Leu Ala
 1 5 10 15

Thr Ile Ser Leu Ser Leu Ser Thr Cys Thr Thr Leu Asp Phe Gly His
 20 25 30

Ile Lys Lys Lys Arg Val Glu Ala Ile Arg Gly Gln Ile Leu Ser Lys
 35 40 45

Leu Arg Leu Thr Ser Pro Pro Glu Pro Ser Val Met Thr His Val Pro
50 55 60

Tyr Gln Val Leu Ala Leu Tyr Asn Ser Thr Arg Glu Leu Leu Glu Glu
65 70 75 80

Met His Gly Glu Arg Glu Glu Gly Cys Thr Gln Glu Thr Ser Glu Ser
85 90 95

Glu Tyr Tyr Ala Lys Glu Ile His Lys Phe Asp Met Ile Gln Gly Leu
100 105 110

Ala Glu His Asn Glu Leu Ala Val Cys Pro Lys Gly Ile Thr Ser Lys
115 120 125

Val Phe Arg Phe Asn Val Ser Ser Val Glu Lys Asn Gly Thr Asn Leu
130 135 140

Phe Arg Ala Glu Phe Arg Val Leu Arg Val Pro Asn Pro Ser Ser Lys
145 150 155 160

Arg Thr Glu Gln Arg Ile Glu Leu Phe Gln Ile Leu Arg Pro Asp Glu
165 170 175

His Ile Ala Lys Gln Arg Tyr Ile Gly Gly Lys Asn Leu Pro Thr Arg
180 185 190

Gly Thr Ala Glu Trp Leu Ser Phe Asp Val Thr Asp Thr Val Arg Glu
195 200 205

Trp Leu Leu Arg Arg Glu Ser Asn Leu Gly Leu Glu Ile Ser Ile His
210 215 220

Cys Pro Cys His Thr Phe Gln Pro Asn Gly Asp Ile Leu Glu Asn Val
225 230 235 240

His Glu Val Met Glu Ile Lys Phe Lys Gly Val Asp Asn Glu Asp Asp
245 250 255

His Gly Arg Gly Asp Leu Gly Arg Leu Lys Lys Gln Lys Asp His His
260 265 270

Asn Pro His Leu Ile Leu Met Met Ile Pro Pro His Arg Leu Asp Ser
275 280 285

Pro Gly Gln Gly Ser Gln Arg Lys Lys Arg Ala Leu Asp Thr Asn Asp
290 295 300

Tyr Lys Asp Asp Asp Asp Lys Ala Leu Asp Thr Asn Tyr Cys Phe Arg
305 310 315 320

Asn Leu Glu Glu Asn Cys Cys Val Arg Pro Leu Tyr Ile Asp Phe Arg
325 330 335

Gln Asp Leu Gly Trp Lys Trp Val His Glu Pro Lys Gly Tyr Tyr Ala
340 345 350

Asn Phe Cys Ser Gly Pro Cys Pro Tyr Leu Arg Ser Ala Asp Thr Thr
355 360 365

His Ser Thr Val Leu Gly Leu Tyr Asn Thr Leu Asn Pro Glu Ala Ser
370 375 380

Ala Ser Pro Cys Cys Val Pro Gln Asp Leu Glu Pro Leu Thr Ile Leu
385 390 395 400

Tyr Tyr Val Gly Arg Thr Pro Lys Val Glu Gln Leu Ser Asn Met Val
405 410 415

Val Lys Ser Cys Lys Cys Ser
420

<210> 30
<211> 1284
<212> DNA
<213> Artificial Sequence

<220>
<223> Murine (Mus musculus) TGF-beta3/N+5 HA Fusion Construct

<220>
<221> CDS
<222> (1)..(1284)
<223> Protein coding sequence

<220>
<221> misc_feature

<222> (895)..(909)
 <223> Encodes amino acid residues 1-5 of TGF-beta3

<220>
 <221> misc_feature
 <222> (895)..(1284)
 <223> Encodes mature fusion protein

<220>
 <221> misc_feature
 <222> (910)..(945)
 <223> Encodes HA epitope tag

<400> 30
 atg cac ttg caa agg gct ctg gta gtc ctg gcc ctg ctg aac ttg gcc 48
 Met His Leu Gln Arg Ala Leu Val Val Leu Ala Leu Leu Asn Leu Ala
 1 5 10 15

aca atc agc ctc tct ctg tcc act tgc acc acg ttg gac ttc ggc cac 96
 Thr Ile Ser Leu Ser Leu Ser Thr Cys Thr Thr Leu Asp Phe Gly His
 20 25 30

atc aag aag aag agg gtg gaa gcc att agg gga cag atc ttg agc aag 144
 Ile Lys Lys Lys Arg Val Glu Ala Ile Arg Gly Gln Ile Leu Ser Lys
 35 40 45

ctc agg ctc acc agc ccc cct gag cca tcg gtg atg acc cac gtc ccc 192
 Leu Arg Leu Thr Ser Pro Pro Glu Pro Ser Val Met Thr His Val Pro
 50 55 60

C1 tat cag gtc ctg gca ctt tac aac agc acc cgg gag ttg ctg gaa gag 240
 Tyr Gln Val Leu Ala Leu Tyr Asn Ser Thr Arg Glu Leu Leu Glu Glu
 65 70 75 80

atg cac ggg gag agg gag gaa ggc tgc act cag gag acc tcg gag tct 288
 Met His Gly Glu Arg Glu Glu Gly Cys Thr Gln Glu Thr Ser Glu Ser
 85 90 95

gag tac tat gcc aaa gag atc cat aaa ttc gac atg atc cag gga ctg 336
 Glu Tyr Tyr Ala Lys Glu Ile His Lys Phe Asp Met Ile Gln Gly Leu
 100 105 110

gcg gag cac aat gaa ctg gcc gtc tgc ccc aaa gga att acc tct aag 384
 Ala Glu His Asn Glu Leu Ala Val Cys Pro Lys Gly Ile Thr Ser Lys
 115 120 125

gtt ttt cgt ttc aat gtg tcc tca gtg gag aaa aat gga acc aat ctg 432
 Val Phe Arg Phe Asn Val Ser Ser Val Glu Lys Asn Gly Thr Asn Leu
 130 135 140

ttc cgg gca gag ttc cgg gtc ttg cgg gtg ccc aac ccc agc tcc aag 480
 Phe Arg Ala Glu Phe Arg Val Leu Arg Val Pro Asn Pro Ser Ser Lys
 145 150 155 160

cgc aca gag cag aga att gag ctc ttc cag ata ctt cga ccg gat gag 528
 Arg Thr Glu Gln Arg Ile Glu Leu Phe Gln Ile Leu Arg Pro Asp Glu
 165 170 175

cac ata gcc aag cag cgc tac ata ggt ggc aag aat ctg ccc aca agg	576
His Ile Ala Lys Gln Arg Tyr Ile Gly Gly Lys Asn Leu Pro Thr Arg	
180 185 190	
ggc acc gct gaa tgg ctg tct ttc gat gtc act gac act gtg cgc gag	624
Gly Thr Ala Glu Trp Leu Ser Phe Asp Val Thr Asp Thr Val Arg Glu	
195 200 205	
tgg ctg ttg agg aga gag tcc aac ttg ggt ctg gaa atc agc atc cac	672
Trp Leu Leu Arg Arg Glu Ser Asn Leu Gly Leu Glu Ile Ser Ile His	
210 215 220	
tgt cca tgt cac acc ttt cag ccc aat gga gac ata ctg gaa aat gtt	720
Cys Pro Cys His Thr Phe Gln Pro Asn Gly Asp Ile Leu Glu Asn Val	
225 230 235 240	
cat gag gtg atg gaa atc aaa ttc aaa gga gtg gac aat gaa gat gac	768
His Glu Val Met Glu Ile Lys Phe Lys Gly Val Asp Asn Glu Asp Asp	
245 250 255	
cat ggc cgt gga gac ctg ggg cgt ctc aag aag caa aag gat cac cac	816
His Gly Arg Gly Asp Leu Gly Arg Leu Lys Lys Gln Lys Asp His His	
260 265 270	
aac cca cac ctg atc ctc atg atg atc ccc cca cac cga ctg gac agc	864
Asn Pro His Leu Ile Leu Met Met Ile Pro Pro His Arg Leu Asp Ser	
275 280 285	
cca ggc cag ggc agt cag agg aag aag agg gcc ctg gac acc aat agc	912
Pro Gly Gln Gly Ser Gln Arg Lys Lys Arg Ala Leu Asp Thr Asn Ser	
290 295 300	
tac cca tac gac gtg cca gac tac gca tct ctg gcc ctg gac acc aat	960
Tyr Pro Tyr Asp Val Pro Asp Tyr Ala Ser Leu Ala Leu Asp Thr Asn	
305 310 315 320	
tac tgc ttc cgc aac ctg gag gag aac tgc tgt gta cgc ccc ctt tat	1008
Tyr Cys Phe Arg Asn Leu Glu Glu Asn Cys Cys Val Arg Pro Leu Tyr	
325 330 335	
att gac ttc cgg cag gat cta ggc tgg aaa tgg gtc cac gaa cct aag	1056
Ile Asp Phe Arg Gln Asp Leu Gly Trp Lys Trp Val His Glu Pro Lys	
340 345 350	
ggg tac tat gcc aac ttc tgc tca ggc cct tgc cca tac ctc cgc agc	1104
Gly Tyr Tyr Ala Asn Phe Cys Ser Gly Pro Cys Pro Tyr Leu Arg Ser	
355 360 365	
gca gac aca acc cat agc acg gtg ctt gga cta tac aac acc ctg aac	1152
Ala Asp Thr Thr His Ser Thr Val Leu Gly Leu Tyr Asn Thr Leu Asn	
370 375 380	
cca gag gcg tct gcc tcg cca tgc tgc gtc ccc cag gac ctg gag ccc	1200
Pro Glu Ala Ser Ala Ser Pro Cys Cys Val Pro Gln Asp Leu Glu Pro	
385 390 395 400	

ctg acc atc ttg tac tat gtg ggc aga acc ccc aag gtg gag cag ctg 1248
 Leu Thr Ile Leu Tyr Tyr Val Gly Arg Thr Pro Lys Val Glu Gln Leu
 405 410 415

tcc aac atg gtg gtg aag tcg tgt aag tgc agc tga 1284
 Ser Asn Met Val Val Lys Ser Cys Lys Cys Ser
 420 425

<210> 31
 <211> 427
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Murine (Mus musculus) TGF-beta3/N+5 HA Fusion Construct

<400> 31

Met His Leu Gln Arg Ala Leu Val Val Leu Ala Leu Leu Asn Leu Ala
 1 5 10 15

Thr Ile Ser Leu Ser Leu Ser Thr Cys Thr Thr Leu Asp Phe Gly His
 20 25 30

Ile Lys Lys Lys Arg Val Glu Ala Ile Arg Gly Gln Ile Leu Ser Lys
 35 40 45

Leu Arg Leu Thr Ser Pro Pro Glu Pro Ser Val Met Thr His Val Pro
 50 55 60

Tyr Gln Val Leu Ala Leu Tyr Asn Ser Thr Arg Glu Leu Leu Glu Glu
 65 70 75 80

Met His Gly Glu Arg Glu Glu Gly Cys Thr Gln Glu Thr Ser Glu Ser
 85 90 95

Glu Tyr Tyr Ala Lys Glu Ile His Lys Phe Asp Met Ile Gln Gly Leu
 100 105 110

Ala Glu His Asn Glu Leu Ala Val Cys Pro Lys Gly Ile Thr Ser Lys
 115 120 125

Val Phe Arg Phe Asn Val Ser Ser Val Glu Lys Asn Gly Thr Asn Leu
 130 135 140

Phe Arg Ala Glu Phe Arg Val Leu Arg Val Pro Asn Pro Ser Ser Lys
 145 150 155 160

C1

Arg Thr Glu Gln Arg Ile Glu Leu Phe Gln Ile Leu Arg Pro Asp Glu
165 170 175

His Ile Ala Lys Gln Arg Tyr Ile Gly Gly Lys Asn Leu Pro Thr Arg
180 185 190

Gly Thr Ala Glu Trp Leu Ser Phe Asp Val Thr Asp Thr Val Arg Glu
195 200 205

Trp Leu Leu Arg Arg Glu Ser Asn Leu Gly Leu Glu Ile Ser Ile His
210 215 220

Cys Pro Cys His Thr Phe Gln Pro Asn Gly Asp Ile Leu Glu Asn Val
225 230 235 240

His Glu Val Met Glu Ile Lys Phe Lys Gly Val Asp Asn Glu Asp Asp
245 250 255

His Gly Arg Gly Asp Leu Gly Arg Leu Lys Lys Gln Lys Asp His His
260 265 270

Asn Pro His Leu Ile Leu Met Met Ile Pro Pro His Arg Leu Asp Ser
275 280 285

Pro Gly Gln Gly Ser Gln Arg Lys Lys Arg Ala Leu Asp Thr Asn Ser
290 295 300

Tyr Pro Tyr Asp Val Pro Asp Tyr Ala Ser Leu Ala Leu Asp Thr Asn
305 310 315 320

Tyr Cys Phe Arg Asn Leu Glu Glu Asn Cys Cys Val Arg Pro Leu Tyr
325 330 335

Ile Asp Phe Arg Gln Asp Leu Gly Trp Lys Trp Val His Glu Pro Lys
340 345 350

Gly Tyr Tyr Ala Asn Phe Cys Ser Gly Pro Cys Pro Tyr Leu Arg Ser
355 360 365

Ala Asp Thr Thr His Ser Thr Val Leu Gly Leu Tyr Asn Thr Leu Asn
370 375 380

Pro Glu Ala Ser Ala Ser Pro Cys Cys Val Pro Gln Asp Leu Glu Pro
 385 390 395 400

Leu Thr Ile Leu Tyr Tyr Val Gly Arg Thr Pro Lys Val Glu Gln Leu
 405 410 415

Ser Asn Met Val Val Lys Ser Cys Lys Cys Ser
 420 425

<210> 32
 <211> 1349
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Porcine (Sus scrofa) TGF-beta1/N+5 FLAG Fusion Construct

<220>
 <221> 5'UTR
 <222> (1)..(10)
 <223> 5' untranslated region

<220>
 <221> CDS
 <222> (11)..(1222)
 <223> Protein coding sequence

<220>
 <221> misc_feature
 <222> (845)..(859)
 <223> Encodes amino acid residues 1-5 of TGF-beta1

<220>
 <221> misc_feature
 <222> (845)..(1222)
 <223> Encodes mature fusion protein

<220>
 <221> misc_feature
 <222> (860)..(883)
 <223> Encodes FLAG epitope tag

<220>
 <221> 3'UTR
 <222> (1223)..(1349)
 <223> 3' untranslated region

<400> 32
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 Met Ala Pro Ser Gly Leu Arg Leu Leu Pro Leu Leu Leu
 1 5 10

49

ccg ctg ctg tgg ctg cta gtg ctg acg cct ggc cgg ccg gcc gcc gga Pro Leu Leu Trp Leu Leu Val Leu Thr Pro Gly Arg Pro Ala Ala Gly 15 20 25	97
ctg tcc acc tgc aag acc atc gac atg gag ctg gtg aag cgg aag cgc Leu Ser Thr Cys Lys Thr Ile Asp Met Glu Leu Val Lys Arg Lys Arg 30 35 40 45	145
atc gag gcc att cgc ggc cag att ctg tcc aag ctt cgg ctt gcc agc Ile Glu Ala Ile Arg Gly Gln Ile Leu Ser Lys Leu Arg Leu Ala Ser 50 55 60	193
ccc ccg agc cag ggg gac gtg ccg ccc ggc ccg ctg cct gag gca gta Pro Pro Ser Gln Gly Asp Val Pro Pro Gly Pro Leu Pro Glu Ala Val 65 70 75	241
ctg gct ctt tac aac agt acc cgc gac cgg gta gcc ggg gaa agt gtc Leu Ala Leu Tyr Asn Ser Thr Arg Asp Arg Val Ala Gly Glu Ser Val 80 85 90	289
gaa ccg gag ccc gag cca gag gcg gac tac tac gcc aag gag gtc acc Glu Pro Glu Pro Glu Pro Glu Ala Asp Tyr Tyr Ala Lys Glu Val Thr 95 100 105	337
cgc gtg cta atg gtg gaa agc ggc aac caa atc tat gat aaa ttc aag Arg Val Leu Met Val Glu Ser Gly Asn Gln Ile Tyr Asp Lys Phe Lys 110 115 120 125	385
ggc acc ccc cac agc tta tat atg ctg ttc aac acg tcg gag ctc cgg Gly Thr Pro His Ser Leu Tyr Met Leu Phe Asn Thr Ser Glu Leu Arg 130 135 140	433
gaa gcg gtg ccg gaa cct gta ttg ctc tct cgg gca gag ctg cgc ctg Glu Ala Val Pro Glu Pro Val Leu Leu Ser Arg Ala Glu Leu Arg Leu 145 150 155	481
ctg agg ctc aag tta aaa gtg gag cag cac gtg gag cta tac cag aaa Leu Arg Leu Lys Leu Lys Val Glu Gln His Val Glu Leu Tyr Gln Lys 160 165 170	529
tac agc aat gat tcc tgg cgc tac ctc agc aac cgg ctg ctg gcc ccc Tyr Ser Asn Asp Ser Trp Arg Tyr Leu Ser Asn Arg Leu Leu Ala Pro 175 180 185	577
agt gac tca ccg gag tgg ctg tcc ttt gat gtc acc gga gtt gtg cgg Ser Asp Ser Pro Glu Trp Leu Ser Phe Asp Val Thr Gly Val Val Arg 190 195 200 205	625
cag tgg ctg acc cgc aga gag gct ata gag ggt ttt cgc ctc agt gcc Gln Trp Leu Thr Arg Arg Glu Ala Ile Glu Gly Phe Arg Leu Ser Ala 210 215 220	673
cac tct tcc tct gac agc aaa gat aac aca ctc cac gtg gaa att aac His Ser Ser Ser Asp Ser Lys Asp Asn Thr Leu His Val Glu Ile Asn 225 230 235	721
ggg ttc aat tct ggc cgc cgg ggt gac ctg gcc acc att cac ggc atg	769

Gly	Phe	Asn	Ser	Gly	Arg	Arg	Gly	Asp	Leu	Ala	Thr	Ile	His	Gly	Met	
		240					245					250				
aac	cg	ccc	ttc	ctg	ctc	ctc	atg	gcc	acc	ccg	ctg	gag	agg	gcc	cag	817
Asn	Arg	Pro	Phe	Leu	Leu	Leu	Met	Ala	Thr	Pro	Leu	Glu	Arg	Ala	Gln	
		255					260				265					
cac	ctg	cac	agc	tcc	cgg	cac	cgc	cga	gcc	ctg	gat	acc	aac	gac	tac	865
His	Leu	His	Ser	Ser	Arg	His	Arg	Arg	Ala	Leu	Asp	Thr	Asn	Asp	Tyr	
		270				275				280					285	
aag	gat	gac	gac	gac	aag	gcc	ctg	gat	acc	aac	tac	tgc	ttc	agc	tcc	913
Lys	Asp	Asp	Asp	Asp	Lys	Ala	Leu	Asp	Thr	Asn	Tyr	Cys	Phe	Ser	Ser	
					290				295					300		
acg	gag	aag	aac	tgc	tgc	gtg	cgg	cag	ctc	tac	att	gac	ttc	cgg	aag	961
Thr	Glu	Lys	Asn	Cys	Cys	Val	Arg	Gln	Leu	Tyr	Ile	Asp	Phe	Arg	Lys	
			305					310					315			
gac	ctg	ggc	tgg	aag	tgg	att	cat	gaa	ccc	aag	ggc	tac	cat	gcc	aat	1009
Asp	Leu	Gly	Trp	Lys	Trp	Ile	His	Glu	Pro	Lys	Gly	Tyr	His	Ala	Asn	
		320					325					330				
ttc	tgc	ctg	ggg	ccc	tgt	ccc	tac	atc	tgg	agc	cta	gac	act	cag	tac	1057
Phe	Cys	Leu	Gly	Pro	Cys	Pro	Tyr	Ile	Trp	Ser	Leu	Asp	Thr	Gln	Tyr	
		335				340					345					
agc	aag	gtc	ctg	gct	ctg	tac	aac	cag	cac	aac	ccg	ggc	gcg	tcg	gcg	1105
Ser	Lys	Val	Leu	Ala	Leu	Tyr	Asn	Gln	His	Asn	Pro	Gly	Ala	Ser	Ala	
		350			355					360					365	
cg	ccg	tgc	tgc	gtg	ccg	cag	gcg	ctg	gag	cca	ctg	ccc	atc	gtg	tac	1153
Ala	Pro	Cys	Cys	Val	Pro	Gln	Ala	Leu	Glu	Pro	Leu	Pro	Ile	Val	Tyr	
				370				375					380			
tac	gtg	ggc	cgc	aag	ccc	aag	gtg	gag	cag	ctg	tcc	aac	atg	atc	gtg	1201
Tyr	Val	Gly	Arg	Lys	Pro	Lys	Val	Glu	Gln	Leu	Ser	Asn	Met	Ile	Val	
			385				390					395				
cgt	tcc	tgc	aag	tgc	agc	tga	ggccccgccc	cgccccacagc	ccccgcccacc							1252
Arg	Ser	Cys	Lys	Cys	Ser											
			400													
cg	gag	ggc	ggccccacccc	ccgccccgcct	caccgggggt	gtattttaagg	acatcg	gtgcc								1312
cca	agccccac	ttgggatcga	ttaaagcggc	cgcgact												1349

<210> 33
 <211> 403
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Porcine (Sus scrofa) TGF-beta1/N+5 FLAG Fusion Construct

<400> 33

Met Ala Pro Ser Gly Leu Arg Leu Leu Pro Leu Leu Leu Pro Leu Leu
1 5 10 15

Trp Leu Leu Val Leu Thr Pro Gly Arg Pro Ala Ala Gly Leu Ser Thr
20 25 30

Cys Lys Thr Ile Asp Met Glu Leu Val Lys Arg Lys Arg Ile Glu Ala
35 40 45

Ile Arg Gly Gln Ile Leu Ser Lys Leu Arg Leu Ala Ser Pro Pro Ser
50 55 60

Gln Gly Asp Val Pro Pro Gly Pro Leu Pro Glu Ala Val Leu Ala Leu
65 70 75 80

Tyr Asn Ser Thr Arg Asp Arg Val Ala Gly Glu Ser Val Glu Pro Glu
85 90 95

Pro Glu Pro Glu Ala Asp Tyr Tyr Ala Lys Glu Val Thr Arg Val Leu
100 105 110

Met Val Glu Ser Gly Asn Gln Ile Tyr Asp Lys Phe Lys Gly Thr Pro
115 120 125

His Ser Leu Tyr Met Leu Phe Asn Thr Ser Glu Leu Arg Glu Ala Val
130 135 140

Pro Glu Pro Val Leu Leu Ser Arg Ala Glu Leu Arg Leu Leu Arg Leu
145 150 155 160

Lys Leu Lys Val Glu Gln His Val Glu Leu Tyr Gln Lys Tyr Ser Asn
165 170 175

Asp Ser Trp Arg Tyr Leu Ser Asn Arg Leu Leu Ala Pro Ser Asp Ser
180 185 190

Pro Glu Trp Leu Ser Phe Asp Val Thr Gly Val Val Arg Gln Trp Leu
195 200 205

Thr Arg Arg Glu Ala Ile Glu Gly Phe Arg Leu Ser Ala His Ser Ser
210 215 220

Ser Asp Ser Lys Asp Asn Thr Leu His Val Glu Ile Asn Gly Phe Asn
225 230 235 240

Ser Gly Arg Arg Gly Asp Leu Ala Thr Ile His Gly Met Asn Arg Pro
245 250 255

Phe Leu Leu Leu Met Ala Thr Pro Leu Glu Arg Ala Gln His Leu His
260 265 270

Ser Ser Arg His Arg Arg Ala Leu Asp Thr Asn Asp Tyr Lys Asp Asp
275 280 285

Asp Asp Lys Ala Leu Asp Thr Asn Tyr Cys Phe Ser Ser Thr Glu Lys
290 295 300

Asn Cys Cys Val Arg Gln Leu Tyr Ile Asp Phe Arg Lys Asp Leu Gly
305 310 315 320

Trp Lys Trp Ile His Glu Pro Lys Gly Tyr His Ala Asn Phe Cys Leu
325 330 335

Gly Pro Cys Pro Tyr Ile Trp Ser Leu Asp Thr Gln Tyr Ser Lys Val
340 345 350

Leu Ala Leu Tyr Asn Gln His Asn Pro Gly Ala Ser Ala Ala Pro Cys
355 360 365

Cys Val Pro Gln Ala Leu Glu Pro Leu Pro Ile Val Tyr Tyr Val Gly
370 375 380

Arg Lys Pro Lys Val Glu Gln Leu Ser Asn Met Ile Val Arg Ser Cys
385 390 395 400

Lys Cys Ser

<210> 34

<211> 1353

<212> DNA

<213> Artificial Sequence

<220>

<223> Porcine (Sus scrofa) TGF-beta1/N+5 FLAG Fusion Construct

<220>
 <221> 5'utr
 <222> (1)..(14)
 <223> 5' untranslated region

 <220>
 <221> CDS
 <222> (15)..(1226)
 <223> Protein coding sequence

 <220>
 <221> misc_feature
 <222> (849)..(863)
 <223> Encodes amino acid residues 1-5 of TGF-beta1

 <220>
 <221> misc_feature
 <222> (849)..(1226)
 <223> Encodes mature fusion protein

 <220>
 <221> misc_feature
 <222> (864)..(887)
 <223> Encodes FLAG epitope tage

 <220>
 <221> 3'UTR
 <222> (1227)..(1353)
 <223> 3' untranslated region

C1
 <400> 34
 gatctggtac cgag atg gcg cct tgc ggg ctg cgg ctc ttg ccg ctg ctg 50
 Met Ala Pro Ser Gly Leu Arg Leu Leu Pro Leu Leu
 1 5 10

 ctg ccg ctg ctg tgg ctg cta gtg ctg acg cct ggc cgg ccg gcc gcc 98
 Leu Pro Leu Leu Trp Leu Leu Val Leu Thr Pro Gly Arg Pro Ala Ala
 15 20 25

 gga ctg tcc acc tgc aag acc atc gac atg gag ctg gtg aag cgg aag 146
 Gly Leu Ser Thr Cys Lys Thr Ile Asp Met Glu Leu Val Lys Arg Lys
 30 35 40

 cgc atc gag gcc att cgc ggc cag att ctg tcc aag ctt cgg ctt gcc 194
 Arg Ile Glu Ala Ile Arg Gly Gln Ile Leu Ser Lys Leu Arg Leu Ala
 45 50 55 60

 agc ccc ccg agc cag ggg gac gtg ccg ccc ggc ccg ctg cct gag gca 242
 Ser Pro Pro Ser Gln Gly Asp Val Pro Pro Gly Pro Leu Pro Glu Ala
 65 70 75

 gta ctg gct ctt tac aac agt acc cgc gac cgg gta gcc ggg gaa agt 290
 Val Leu Ala Leu Tyr Asn Ser Thr Arg Asp Arg Val Ala Gly Glu Ser
 80 85 90

 gtc gaa ccg gag ccc gag cca gag gcg gac tac tac gcc aag gag gtc 338
 Val Glu Pro Glu Pro Glu Pro Glu Ala Asp Tyr Tyr Ala Lys Glu Val

95	100	105	
acc cgc gtg cta atg gtg gaa agc ggc aac caa atc tat gat aaa ttc			386
Thr Arg Val Leu Met Val Glu Ser Gly Asn Gln Ile Tyr Asp Lys Phe			
110	115	120	
aag ggc acc ccc cac agc tta tat atg ctg ttc aac acg tcg gag ctc			434
Lys Gly Thr Pro His Ser Leu Tyr Met Leu Phe Asn Thr Ser Glu Leu			
125	130	135	140
cgg gaa gcg gtg ccg gaa cct gta ttg ctc tct cgg gca gag ctg cgc			482
Arg Glu Ala Val Pro Glu Pro Val Leu Leu Ser Arg Ala Glu Leu Arg			
	145	150	155
ctg ctg agg ctc aag tta aaa gtg gag cag cac gtg gag cta tac cag			530
Leu Leu Arg Leu Lys Leu Lys Val Glu Gln His Val Glu Leu Tyr Gln			
	160	165	170
aaa tac agc aat gat tcc tgg cgc tac ctc agc aac cgg ctg ctg gcc			578
Lys Tyr Ser Asn Asp Ser Trp Arg Tyr Leu Ser Asn Arg Leu Leu Ala			
	175	180	185
ccc agt gac tca ccg gag tgg ctg tcc ttt gat gtc acc gga gtt gtg			626
Pro Ser Asp Ser Pro Glu Trp Leu Ser Phe Asp Val Thr Gly Val Val			
	190	195	200
cgg cag tgg ctg acc cgc aga gag gct ata gag ggt ttt cgc ctc agt			674
Arg Gln Trp Leu Thr Arg Arg Glu Ala Ile Glu Gly Phe Arg Leu Ser			
205	210	215	220
gcc cac tgt tcc tgt gac agc aaa gat aac aca ctc cac gtg gaa att			722
Ala His Cys Ser Cys Asp Ser Lys Asp Asn Thr Leu His Val Glu Ile			
	225	230	235
aac ggg ttc aat tct ggc cgc cgg ggt gac ctg gcc acc att cac ggc			770
Asn Gly Phe Asn Ser Gly Arg Arg Gly Asp Leu Ala Thr Ile His Gly			
	240	245	250
atg aac cgg ccc ttc ctg ctc ctc atg gcc acc ccg ctg gag agg gcc			818
Met Asn Arg Pro Phe Leu Leu Met Ala Thr Pro Leu Glu Arg Ala			
	255	260	265
cag cac ctg cac agc tcc cgg cac cgc cga gcc ctg gat acc aac gac			866
Gln His Leu His Ser Ser Arg His Arg Arg Ala Leu Asp Thr Asn Asp			
	270	275	280
tac aag gat gac gac gac aag gcc ctg gat acc aac tac tgc ttc agc			914
Tyr Lys Asp Asp Asp Asp Lys Ala Leu Asp Thr Asn Tyr Cys Phe Ser			
285	290	295	300
tcc acg gag aag aac tgc tgc gtg cgg cag ctc tac att gac ttc cgg			962
Ser Thr Glu Lys Asn Cys Cys Val Arg Gln Leu Tyr Ile Asp Phe Arg			
	305	310	315
aag gac ctg ggc tgg aag tgg att cat gaa ccc aag ggc tac cat gcc			1010
Lys Asp Leu Gly Trp Lys Trp Ile His Glu Pro Lys Gly Tyr His Ala			
	320	325	330

aat ttc tgc ctg ggg ccc tgt ccc tac atc tgg agc cta gac act cag 1058
 Asn Phe Cys Leu Gly Pro Cys Pro Tyr Ile Trp Ser Leu Asp Thr Gln
 335 340 345

tac agc aag gtc ctg gct ctg tac aac cag cac aac ccg ggc gcg tcg 1106
 Tyr Ser Lys Val Leu Ala Leu Tyr Asn Gln His Asn Pro Gly Ala Ser
 350 355 360

gcg gcg ccg tgc tgc gtg ccg cag gcg ctg gag cca ctg ccc atc gtg 1154
 Ala Ala Pro Cys Cys Val Pro Gln Ala Leu Glu Pro Leu Pro Ile Val
 365 370 375 380

tac tac gtg ggc cgc aag ccc aag gtg gag cag ctg tcc aac atg atc 1202
 Tyr Tyr Val Gly Arg Lys Pro Lys Val Glu Gln Leu Ser Asn Met Ile
 385 390 395

gtg cgt tcc tgc aag tgc agc tga ggccccgccc cgcccacagc cccgcccacc 1256
 Val Arg Ser Cys Lys Cys Ser
 400

cggcaggccc ggccccaccc ccgcccgcct caccgggggt gtatttaagg acatcgtgcc 1316
 ccaagcccac ttgggatcga ttaaagcggc cgcgact 1353

<210> 35
 <211> 403
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Porcine (Sus scrofa) TGF-beta1/N+5 FLAG Fusion Construct
 <400> 35

Met Ala Pro Ser Gly Leu Arg Leu Leu Pro Leu Leu Leu Pro Leu Leu
 1 5 10 15

Trp Leu Leu Val Leu Thr Pro Gly Arg Pro Ala Ala Gly Leu Ser Thr
 20 25 30

Cys Lys Thr Ile Asp Met Glu Leu Val Lys Arg Lys Arg Ile Glu Ala
 35 40 45

Ile Arg Gly Gln Ile Leu Ser Lys Leu Arg Leu Ala Ser Pro Pro Ser
 50 55 60

Gln Gly Asp Val Pro Pro Gly Pro Leu Pro Glu Ala Val Leu Ala Leu
 65 70 75 80

Tyr Asn Ser Thr Arg Asp Arg Val Ala Gly Glu Ser Val Glu Pro Glu

C1

85

90

95

Pro Glu Pro Glu Ala Asp Tyr Tyr Ala Lys Glu Val Thr Arg Val Leu
 100 105 110

Met Val Glu Ser Gly Asn Gln Ile Tyr Asp Lys Phe Lys Gly Thr Pro
 115 120 125

His Ser Leu Tyr Met Leu Phe Asn Thr Ser Glu Leu Arg Glu Ala Val
 130 135 140

Pro Glu Pro Val Leu Leu Ser Arg Ala Glu Leu Arg Leu Leu Arg Leu
 145 150 155 160

Lys Leu Lys Val Glu Gln His Val Glu Leu Tyr Gln Lys Tyr Ser Asn
 165 170 175

Asp Ser Trp Arg Tyr Leu Ser Asn Arg Leu Leu Ala Pro Ser Asp Ser
 180 185 190

Pro Glu Trp Leu Ser Phe Asp Val Thr Gly Val Val Arg Gln Trp Leu
 195 200 205

Thr Arg Arg Glu Ala Ile Glu Gly Phe Arg Leu Ser Ala His Cys Ser
 210 215 220

Cys Asp Ser Lys Asp Asn Thr Leu His Val Glu Ile Asn Gly Phe Asn
 225 230 235 240

Ser Gly Arg Arg Gly Asp Leu Ala Thr Ile His Gly Met Asn Arg Pro
 245 250 255

Phe Leu Leu Leu Met Ala Thr Pro Leu Glu Arg Ala Gln His Leu His
 260 265 270

Ser Ser Arg His Arg Arg Ala Leu Asp Thr Asn Asp Tyr Lys Asp Asp
 275 280 285

Asp Asp Lys Ala Leu Asp Thr Asn Tyr Cys Phe Ser Ser Thr Glu Lys
 290 295 300

Asn Cys Cys Val Arg Gln Leu Tyr Ile Asp Phe Arg Lys Asp Leu Gly
 305 310 315 320

Trp Lys Trp Ile His Glu Pro Lys Gly Tyr His Ala Asn Phe Cys Leu
 325 330 335

Gly Pro Cys Pro Tyr Ile Trp Ser Leu Asp Thr Gln Tyr Ser Lys Val
 340 345 350

Leu Ala Leu Tyr Asn Gln His Asn Pro Gly Ala Ser Ala Ala Pro Cys
 355 360 365

Cys Val Pro Gln Ala Leu Glu Pro Leu Pro Ile Val Tyr Tyr Val Gly
 370 375 380

Arg Lys Pro Lys Val Glu Gln Leu Ser Asn Met Ile Val Arg Ser Cys
 385 390 395 400

Lys Cys Ser

<210> 36
 <211> 1361
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Porcine (Sus scrofa) TGF-beta1/N+5 HA Fusion Construct

<220>
 <221> 5'UTR
 <222> (1)..(10)
 <223> 5' untranslated region

<220>
 <221> CDS
 <222> (11)..(1234)
 <223> Protein coding sequence

<220>
 <221> misc_feature
 <222> (845)..(859)
 <223> Encodes amino acid residues 1-5 of TGF-beta1

<220>
 <221> misc_feature
 <222> (845)..(1234)
 <223> Encodes mature fusion protein

<220>
 <221> misc_feature

<222> (860)..(895)
 <223> Encodes HA epitope tag

<220>
 <221> 3'UTR
 <222> (1235)..(1361)
 <223> 3' untranslated region

<400> 36
 tgggtaccgag atg gcg cct tcg ggg ctg cgg ctc ttg ccg ctg ctg ctg 49
 Met Ala Pro Ser Gly Leu Arg Leu Leu Pro Leu Leu Leu
 1 5 10

ccg ctg ctg tgg ctg cta gtg ctg acg cct ggc cgg ccg gcc gcc gga 97
 Pro Leu Leu Trp Leu Leu Val Leu Thr Pro Gly Arg Pro Ala Ala Gly
 15 20 25

ctg tcc acc tgc aag acc atc gac atg gag ctg gtg aag cgg aag cgc 145
 Leu Ser Thr Cys Lys Thr Ile Asp Met Glu Leu Val Lys Arg Lys Arg
 30 35 40 45

atc gag gcc att cgc ggc cag att ctg tcc aag ctt cgg ctt gcc agc 193
 Ile Glu Ala Ile Arg Gly Gln Ile Leu Ser Lys Leu Arg Leu Ala Ser
 50 55 60

ccc ccg agc cag ggg gac gtg ccg ccc ggc ccg ctg cct gag gca gta 241
 Pro Pro Ser Gln Gly Asp Val Pro Pro Gly Pro Leu Pro Glu Ala Val
 65 70 75

C1
 ctg gct ctt tac aac agt acc cgc gac cgg gta gcc ggg gaa agt gtc 289
 Leu Ala Leu Tyr Asn Ser Thr Arg Asp Arg Val Ala Gly Glu Ser Val
 80 85 90

gaa ccg gag ccc gag cca gag gcg gac tac tac gcc aag gag gtc acc 337
 Glu Pro Glu Pro Glu Pro Glu Ala Asp Tyr Tyr Ala Lys Glu Val Thr
 95 100 105

cgc gtg cta atg gtg gaa agc ggc aac caa atc tat gat aaa ttc aag 385
 Arg Val Leu Met Val Glu Ser Gly Asn Gln Ile Tyr Asp Lys Phe Lys
 110 115 120 125

ggc acc ccc cac agc tta tat atg ctg ttc aac acg tcg gag ctc cgg 433
 Gly Thr Pro His Ser Leu Tyr Met Leu Phe Asn Thr Ser Glu Leu Arg
 130 135 140

gaa gcg gtg ccg gaa cct gta ttg ctc tct cgg gca gag ctg cgc ctg 481
 Glu Ala Val Pro Glu Pro Val Leu Leu Ser Arg Ala Glu Leu Arg Leu
 145 150 155

ctg agg ctc aag tta aaa gtg gag cag cac gtg gag cta tac cag aaa 529
 Leu Arg Leu Lys Leu Lys Val Glu Gln His Val Glu Leu Tyr Gln Lys
 160 165 170

tac agc aat gat tcc tgg cgc tac ctc agc aac cgg ctg ctg gcc ccc 577
 Tyr Ser Asn Asp Ser Trp Arg Tyr Leu Ser Asn Arg Leu Leu Ala Pro
 175 180 185

agt gac tca ccg gag tgg ctg tcc ttt gat gtc acc gga gtt gtg cgg	625
Ser Asp Ser Pro Glu Trp Leu Ser Phe Asp Val Thr Gly Val Val Arg	
190 195 200 205	
cag tgg ctg acc cgc aga gag gct ata gag ggt ttt cgc ctc agt gcc	673
Gln Trp Leu Thr Arg Arg Glu Ala Ile Glu Gly Phe Arg Leu Ser Ala	
210 215 220	
cac tct tcc tct gac agc aaa gat aac aca ctc cac gtg gaa att aac	721
His Ser Ser Ser Asp Ser Lys Asp Asn Thr Leu His Val Glu Ile Asn	
225 230 235	
ggg ttc aat tct ggc cgc cgg ggt gac ctg gcc acc att cac ggc atg	769
Gly Phe Asn Ser Gly Arg Arg Gly Asp Leu Ala Thr Ile His Gly Met	
240 245 250	
aac cgg ccc ttc ctg ctc ctc atg gcc acc ccg ctg gag agg gcc cag	817
Asn Arg Pro Phe Leu Leu Leu Met Ala Thr Pro Leu Glu Arg Ala Gln	
255 260 265	
cac ctg cac agc tcc cgg cac cgc cga gcc ctg gat acc aac agc tac	865
His Leu His Ser Ser Arg His Arg Arg Ala Leu Asp Thr Asn Ser Tyr	
270 275 280 285	
cca tac gac gtg cca gac tac gca tct ctg gcc ctg gat acc aac tac	913
Pro Tyr Asp Val Pro Asp Tyr Ala Ser Leu Ala Leu Asp Thr Asn Tyr	
290 295 300	
tgc ttc agc tcc acg gag aag aac tgc tgc gtg cgg cag ctc tac att	961
Cys Phe Ser Ser Thr Glu Lys Asn Cys Cys Val Arg Gln Leu Tyr Ile	
305 310 315	
gac ttc cgg aag gac ctg ggc tgg aag tgg att cat gaa ccc aag ggc	1009
Asp Phe Arg Lys Asp Leu Gly Trp Lys Trp Ile His Glu Pro Lys Gly	
320 325 330	
tac cat gcc aat ttc tgc ctg ggg ccc tgt ccc tac atc tgg agc cta	1057
Tyr His Ala Asn Phe Cys Leu Gly Pro Cys Pro Tyr Ile Trp Ser Leu	
335 340 345	
gac act cag tac agc aag gtc ctg gct ctg tac aac cag cac aac ccg	1105
Asp Thr Gln Tyr Ser Lys Val Leu Ala Leu Tyr Asn Gln His Asn Pro	
350 355 360 365	
ggc gcg tcg gcg gcg ccg tgc tgc gtg ccg cag gcg ctg gag cca ctg	1153
Gly Ala Ser Ala Ala Pro Cys Cys Val Pro Gln Ala Leu Glu Pro Leu	
370 375 380	
ccc atc gtg tac tac gtg ggc cgc aag ccc aag gtg gag cag ctg tcc	1201
Pro Ile Val Tyr Tyr Val Gly Arg Lys Pro Lys Val Glu Gln Leu Ser	
385 390 395	
aac atg atc gtg cgt tcc tgc aag tgc agc tga ggccccgccc cgccccacagc	1254
Asn Met Ile Val Arg Ser Cys Lys Cys Ser	
400 405	
cccccccc ccggcaggccc ggccccacccc ccgcccgcct caccgggggt gtatttaagg	1314

C1

acatcgtgcc ccaagcccac ttgggatcga ttaaagcggc cgcgact

1361

<210> 37

<211> 407

<212> PRT

<213> Artificial Sequence

<220>

<223> Porcine (Sus scrofa) TGF-beta1/N+5 HA Fusion Construct

<400> 37

Met Ala Pro Ser Gly Leu Arg Leu Leu Pro Leu Leu Leu Pro Leu Leu
1 5 10 15

Trp Leu Leu Val Leu Thr Pro Gly Arg Pro Ala Ala Gly Leu Ser Thr
20 25 30

Cys Lys Thr Ile Asp Met Glu Leu Val Lys Arg Lys Arg Ile Glu Ala
35 40 45

Ile Arg Gly Gln Ile Leu Ser Lys Leu Arg Leu Ala Ser Pro Pro Ser
50 55 60

C1 Gln Gly Asp Val Pro Pro Gly Pro Leu Pro Glu Ala Val Leu Ala Leu
65 70 75 80

Tyr Asn Ser Thr Arg Asp Arg Val Ala Gly Glu Ser Val Glu Pro Glu
85 90 95

Pro Glu Pro Glu Ala Asp Tyr Tyr Ala Lys Glu Val Thr Arg Val Leu
100 105 110

Met Val Glu Ser Gly Asn Gln Ile Tyr Asp Lys Phe Lys Gly Thr Pro
115 120 125

His Ser Leu Tyr Met Leu Phe Asn Thr Ser Glu Leu Arg Glu Ala Val
130 135 140

Pro Glu Pro Val Leu Leu Ser Arg Ala Glu Leu Arg Leu Leu Arg Leu
145 150 155 160

Lys Leu Lys Val Glu Gln His Val Glu Leu Tyr Gln Lys Tyr Ser Asn
165 170 175

Asp Ser Trp Arg Tyr Leu Ser Asn Arg Leu Leu Ala Pro Ser Asp Ser
180 185 190

Pro Glu Trp Leu Ser Phe Asp Val Thr Gly Val Val Arg Gln Trp Leu
195 200 205

Thr Arg Arg Glu Ala Ile Glu Gly Phe Arg Leu Ser Ala His Ser Ser
210 215 220

Ser Asp Ser Lys Asp Asn Thr Leu His Val Glu Ile Asn Gly Phe Asn
225 230 235 240

Ser Gly Arg Arg Gly Asp Leu Ala Thr Ile His Gly Met Asn Arg Pro
245 250 255

Phe Leu Leu Leu Met Ala Thr Pro Leu Glu Arg Ala Gln His Leu His
260 265 270

Ser Ser Arg His Arg Arg Ala Leu Asp Thr Asn Ser Tyr Pro Tyr Asp
275 280 285

Val Pro Asp Tyr Ala Ser Leu Ala Leu Asp Thr Asn Tyr Cys Phe Ser
290 295 300

Ser Thr Glu Lys Asn Cys Cys Val Arg Gln Leu Tyr Ile Asp Phe Arg
305 310 315 320

Lys Asp Leu Gly Trp Lys Trp Ile His Glu Pro Lys Gly Tyr His Ala
325 330 335

Asn Phe Cys Leu Gly Pro Cys Pro Tyr Ile Trp Ser Leu Asp Thr Gln
340 345 350

Tyr Ser Lys Val Leu Ala Leu Tyr Asn Gln His Asn Pro Gly Ala Ser
355 360 365

Ala Ala Pro Cys Cys Val Pro Gln Ala Leu Glu Pro Leu Pro Ile Val
370 375 380

Tyr Tyr Val Gly Arg Lys Pro Lys Val Glu Gln Leu Ser Asn Met Ile
385 390 395 400

Val Arg Ser Cys Lys Cys Ser
405

<210> 38
<211> 1361
<212> DNA
<213> Artificial Sequence

<220>
<223> Porcine (Sus scrofa) TGF-beta1/N+5 HA Fusion Construct

<220>
<221> 5'UTR
<222> (1)..(10)
<223> 5' untranslated region

<220>
<221> CDS
<222> (11)..(1234)
<223> Protein coding sequence

<220>
<221> misc_feature
<222> (845)..(859)
<223> Encodes amino acid residues 1-5 of TGF-beta1

<220>
<221> misc_feature
<222> (845)..(1234)
<223> Encodes mature fusion protein

<220>
<221> misc_feature
<222> (860)..(895)
<223> Encodes HA epitope tag

<220>
<221> 3'UTR
<222> (1235)..(1361)
<223> 3' untranslated region

<400> 38
tggtaccgag atg gcg cct tcg ggg ctg cgg ctc ttg ccg ctg ctg ctg 49
Met Ala Pro Ser Gly Leu Arg Leu Leu Pro Leu Leu Leu
1 5 10

ccg ctg ctg tgg ctg cta gtg ctg acg cct ggc cgg ccg gcc gcc gga 97
Pro Leu Leu Trp Leu Leu Val Leu Thr Pro Gly Arg Pro Ala Ala Gly
15 20 25

ctg tcc acc tgc aag acc atc gac atg gag ctg gtg aag cgg aag cgc 145
Leu Ser Thr Cys Lys Thr Ile Asp Met Glu Leu Val Lys Arg Lys Arg
30 35 40 45

atc gag gcc att cgc ggc cag att ctg tcc aag ctt cgg ctt gcc agc 193

C1

Ile	Glu	Ala	Ile	Arg	Gly	Gln	Ile	Leu	Ser	Lys	Leu	Arg	Leu	Ala	Ser		
				50					55					60			
ccc	ccg	agc	cag	ggg	gac	gtg	ccg	ccc	ggc	ccg	ctg	cct	gag	gca	gta		241
Pro	Pro	Ser	Gln	Gly	Asp	Val	Pro	Pro	Gly	Pro	Leu	Pro	Glu	Ala	Val		
			65					70					75				
ctg	gct	ctt	tac	aac	agt	acc	cgc	gac	cgg	gta	gcc	ggg	gaa	agt	gtc		289
Leu	Ala	Leu	Tyr	Asn	Ser	Thr	Arg	Asp	Arg	Val	Ala	Gly	Glu	Ser	Val		
		80					85					90					
gaa	ccg	gag	ccc	gag	cca	gag	gcg	gac	tac	tac	gcc	aag	gag	gtc	acc		337
Glu	Pro	Glu	Pro	Glu	Pro	Glu	Ala	Asp	Tyr	Tyr	Ala	Lys	Glu	Val	Thr		
	95					100					105						
cgc	gtg	cta	atg	gtg	gaa	agc	ggc	aac	caa	atc	tat	gat	aaa	ttc	aag		385
Arg	Val	Leu	Met	Val	Glu	Ser	Gly	Asn	Gln	Ile	Tyr	Asp	Lys	Phe	Lys		
110				115						120					125		
ggc	acc	ccc	cac	agc	tta	tat	atg	ctg	ttc	aac	acg	tcg	gag	ctc	cgg		433
Gly	Thr	Pro	His	Ser	Leu	Tyr	Met	Leu	Phe	Asn	Thr	Ser	Glu	Leu	Arg		
			130						135					140			
gaa	gcg	gtg	ccg	gaa	cct	gta	ttg	ctc	tct	cgg	gca	gag	ctg	cgc	ctg		481
Glu	Ala	Val	Pro	Glu	Pro	Val	Leu	Leu	Ser	Arg	Ala	Glu	Leu	Arg	Leu		
			145				150						155				
ctg	agg	ctc	aag	tta	aaa	gtg	gag	cag	cac	gtg	gag	cta	tac	cag	aaa		529
Leu	Arg	Leu	Lys	Leu	Lys	Val	Glu	Gln	His	Val	Glu	Leu	Tyr	Gln	Lys		
	160					165						170					
C1	tac	agc	aat	gat	tcc	tgg	cgc	tac	ctc	agc	aac	cgg	ctg	ctg	gcc	ccc	577
	Tyr	Ser	Asn	Asp	Ser	Trp	Arg	Tyr	Leu	Ser	Asn	Arg	Leu	Leu	Ala	Pro	
	175					180					185						
agt	gac	tca	ccg	gag	tgg	ctg	tcc	ttt	gat	gtc	acc	gga	gtt	gtg	cgg		625
Ser	Asp	Ser	Pro	Glu	Trp	Leu	Ser	Phe	Asp	Val	Thr	Gly	Val	Val	Arg		
190				195					200					205			
cag	tgg	ctg	acc	cgc	aga	gag	gct	ata	gag	ggg	ttt	cgc	ctc	agt	gcc		673
Gln	Trp	Leu	Thr	Arg	Arg	Glu	Ala	Ile	Glu	Gly	Phe	Arg	Leu	Ser	Ala		
			210					215						220			
cac	tgt	tcc	tgt	gac	agc	aaa	gat	aac	aca	ctc	cac	gtg	gaa	att	aac		721
His	Cys	Ser	Cys	Asp	Ser	Lys	Asp	Asn	Thr	Leu	His	Val	Glu	Ile	Asn		
			225				230					235					
ggg	ttc	aat	tct	ggc	cgc	cgg	ggg	gac	ctg	gcc	acc	att	cac	ggc	atg		769
Gly	Phe	Asn	Ser	Gly	Arg	Arg	Gly	Asp	Leu	Ala	Thr	Ile	His	Gly	Met		
		240					245					250					
aac	cgg	ccc	ttc	ctg	ctc	ctc	atg	gcc	acc	ccg	ctg	gag	agg	gcc	cag		817
Asn	Arg	Pro	Phe	Leu	Leu	Met	Ala	Thr	Pro	Leu	Glu	Arg	Ala	Gln			
	255					260					265						
cac	ctg	cac	agc	tcc	cgg	cac	cgc	cga	gcc	ctg	gat	acc	aac	agc	tac		865
His	Leu	His	Ser	Ser	Arg	His	Arg	Arg	Ala	Leu	Asp	Thr	Asn	Ser	Tyr		

270	275	280	285	
cca tac gac gtg cca gac tac gca tct ctg gcc ctg gat acc aac tac				913
Pro Tyr Asp Val Pro Asp Tyr Ala Ser Leu Ala Leu Asp Thr Asn Tyr	290	295	300	
tgc ttc agc tcc acg gag aag aac tgc tgc gtg cgg cag ctc tac att				961
Cys Phe Ser Ser Thr Glu Lys Asn Cys Cys Val Arg Gln Leu Tyr Ile	305	310	315	
gac ttc cgg aag gac ctg ggc tgg aag tgg att cat gaa ccc aag ggc				1009
Asp Phe Arg Lys Asp Leu Gly Trp Lys Trp Ile His Glu Pro Lys Gly	320	325	330	
tac cat gcc aat ttc tgc ctg ggg ccc tgt ccc tac atc tgg agc cta				1057
Tyr His Ala Asn Phe Cys Leu Gly Pro Cys Pro Tyr Ile Trp Ser Leu	335	340	345	
gac act cag tac agc aag gtc ctg gct ctg tac aac cag cac aac ccg				1105
Asp Thr Gln Tyr Ser Lys Val Leu Ala Leu Tyr Asn Gln His Asn Pro	350	355	360	365
ggc gcg tcg gcg gcg ccg tgc tgc gtg ccg cag gcg ctg gag cca ctg				1153
Gly Ala Ser Ala Ala Pro Cys Cys Val Pro Gln Ala Leu Glu Pro Leu	370	375	380	
ccc atc gtg tac tac gtg ggc cgc aag ccc aag gtg gag cag ctg tcc				1201
Pro Ile Val Tyr Tyr Val Gly Arg Lys Pro Lys Val Glu Gln Leu Ser	385	390	395	
aac atg atc gtg cgt tcc tgc aag tgc agc tga ggccccgccc cgccccacagc				1254
Asn Met Ile Val Arg Ser Cys Lys Cys Ser	400	405		
ccccccacc cggcaggccc ggccccaccc ccgcccgcct caccggggct gtatttaagg				1314
acatcgtgcc ccaagcccac ttgggatcga ttaaagcggc cgcgact				1361

<210> 39
 <211> 407
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Porcine (Sus scrofa) TGF-beta1/N+5 HA Fusion Construct

<400> 39

Met	Ala	Pro	Ser	Gly	Leu	Arg	Leu	Leu	Pro	Leu	Leu	Leu	Pro	Leu	Leu
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Trp	Leu	Leu	Val	Leu	Thr	Pro	Gly	Arg	Pro	Ala	Ala	Gly	Leu	Ser	Thr
			20					25					30		

Cys Lys Thr Ile Asp Met Glu Leu Val Lys Arg Lys Arg Ile Glu Ala
35 40 45

Ile Arg Gly Gln Ile Leu Ser Lys Leu Arg Leu Ala Ser Pro Pro Ser
50 55 60

Gln Gly Asp Val Pro Pro Gly Pro Leu Pro Glu Ala Val Leu Ala Leu
65 70 75 80

Tyr Asn Ser Thr Arg Asp Arg Val Ala Gly Glu Ser Val Glu Pro Glu
85 90 95

Pro Glu Pro Glu Ala Asp Tyr Tyr Ala Lys Glu Val Thr Arg Val Leu
100 105 110

Met Val Glu Ser Gly Asn Gln Ile Tyr Asp Lys Phe Lys Gly Thr Pro
115 120 125

His Ser Leu Tyr Met Leu Phe Asn Thr Ser Glu Leu Arg Glu Ala Val
130 135 140

Pro Glu Pro Val Leu Leu Ser Arg Ala Glu Leu Arg Leu Leu Arg Leu
145 150 155 160

Lys Leu Lys Val Glu Gln His Val Glu Leu Tyr Gln Lys Tyr Ser Asn
165 170 175

Asp Ser Trp Arg Tyr Leu Ser Asn Arg Leu Leu Ala Pro Ser Asp Ser
180 185 190

Pro Glu Trp Leu Ser Phe Asp Val Thr Gly Val Val Arg Gln Trp Leu
195 200 205

Thr Arg Arg Glu Ala Ile Glu Gly Phe Arg Leu Ser Ala His Cys Ser
210 215 220

Cys Asp Ser Lys Asp Asn Thr Leu His Val Glu Ile Asn Gly Phe Asn
225 230 235 240

Ser Gly Arg Arg Gly Asp Leu Ala Thr Ile His Gly Met Asn Arg Pro
245 250 255

Phe Leu Leu Leu Met Ala Thr Pro Leu Glu Arg Ala Gln His Leu His

260

265

270

Ser Ser Arg His Arg Arg Ala Leu Asp Thr Asn Ser Tyr Pro Tyr Asp
 275 280 285

Val Pro Asp Tyr Ala Ser Leu Ala Leu Asp Thr Asn Tyr Cys Phe Ser
 290 295 300

Ser Thr Glu Lys Asn Cys Cys Val Arg Gln Leu Tyr Ile Asp Phe Arg
 305 310 315 320

Lys Asp Leu Gly Trp Lys Trp Ile His Glu Pro Lys Gly Tyr His Ala
 325 330 335

Asn Phe Cys Leu Gly Pro Cys Pro Tyr Ile Trp Ser Leu Asp Thr Gln
 340 345 350

C1 Tyr Ser Lys Val Leu Ala Leu Tyr Asn Gln His Asn Pro Gly Ala Ser
 355 360 365

Ala Ala Pro Cys Cys Val Pro Gln Ala Leu Glu Pro Leu Pro Ile Val
 370 375 380

Tyr Tyr Val Gly Arg Lys Pro Lys Val Glu Gln Leu Ser Asn Met Ile
 385 390 395 400

Val Arg Ser Cys Lys Cys Ser
 405